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## MEMORANDUM

**To:** Robert Law and Willard Potter, de maximis, inc.

**From:** John Tett, Windward Environmental LLC

**cc:** Lisa Sabo and Mike Johnson, Windward Environmental LLC

**Subject:** Response to USEPA request for Specific Additional Information Regarding the LPRSA Bioaccumulation Model

**Date:** April 23, 2015

On March 31, 2015, the US Environmental Protection Agency (USEPA) Region 2 requested specific additional information about the Lower Passaic River Study Area (LPRSA) bioaccumulation model from de maximis. This memorandum provides the information that USEPA Region 2 has requested. Please do not hesitate to contact me if you have any questions or need additional information.

### 1 DATA REDUCTION PROCESS USED FOR FISH TISSUE AND CHEMICAL CONCENTRATION DATA

USEPA requested information regarding the fish tissue samples and averaging used to get the values on the "Empirical Tissue" tab of the steady state model spreadsheet. The fish tissue data used for calibrating the LPRSA bioaccumulation model were collected, composited and analyzed under USEPA direction and oversight.

The bioaccumulation model calibration used the most current empirical whole-body fish and crab tissue data collected from the LPRSA in 2009/2010 (see Tables 1 and 2). Attachment 1 provides further detail on the data selection and rationale for the model calibration. Note that two carp samples collected between RM 4 and RM 5 and one catfish sample collected near RM 2 were not included in the calibration dataset because they were collected from outside the modeling areas (rationale for the selection of modeling areas is discussed in response to Question 2). See Attachment 1 for additional information.

**Table 1. Numbers of tissue samples used in model calibration**

LPRSA Area	Number of Whole-Body Samples											
	Blue Crab		Common Carp		White Perch		Catfish <sup>a</sup>		American Eel		Bass <sup>b</sup>	
	C	I	C	I	C	I	C	I	C	I	C	I
RM 0 – RM 2 (Reach 1)	8	-	-	-	-	2	-	-	1	1	-	-
RM 2 – RM 4 (Reach 2)	6	-	-	-	-	1	-	0 <sup>c</sup>	1	-	-	-
RM 4 – RM 6 (Reach 3)	4	-	-	0 <sup>d</sup>	6	-	-	4	-	3	-	-
RM 6 – RM 8 (Reach 4)	4	-	-	2	2	-	-	1	-	4	1	-
RM 8 – RM 10 (Reach 5)	2	-	-	2	3	-	-	3	1	2	2	1
RM 10 – RM 12 (Reach 6)	-	-	-	2	-	1	-	7	-	2	-	-
RM 12 – RM 14 (Reach 7)	-	-	-	2	1	1	-	4	-	1	-	-
RM 14 – RM 17.4 (Reach 8)	-	-	-	2	3	-	-	10	5	-	1	1
<b>Site-wide total</b>	<b>24</b>	<b>0</b>	<b>0</b>	<b>10</b>	<b>15</b>	<b>5</b>	<b>0</b>	<b>29</b>	<b>8</b>	<b>13</b>	<b>4</b>	<b>2</b>

<sup>a</sup> Includes white catfish and channel catfish.

<sup>b</sup> Includes smallmouth and largemouth bass.

<sup>c</sup> One individual catfish sample was excluded from the calibration dataset because it was collected outside of the modeling area identified for catfish (see Section 3.2.5). This sample was collected near RM 2.2. The sample could have been included because the catfish likely spent most of its time in the modeling area and moved further downstream with a freshwater excursion. The effect of exclusion vs. inclusion was evaluated as an uncertainty and found to be insignificant.

<sup>d</sup> Two individual carp samples were excluded from the calibration dataset because they were collected outside of the modeling area identified for carp (see Section 3.2.5). These samples were collected between RM 5 and RM 6. The two individual carp samples could have been included because the fish likely spent most of their time in the modeling area and moved further downstream with a freshwater excursion. The effect of exclusion vs. inclusion was evaluated as an uncertainty and found to be insignificant.

C – composite fish sample

I – individual fish sample

LPRSA – Lower Passaic River

RM – river mile

**Table 2. Summary of empirical fish and crab tissue concentrations for model calibration**

Model Compartment	Modeling Area	No. of Samples	Concentration (ng/kg ww)					
			2,3,7,8-TCDD		Tetra B		Polychlorinated Biphenyls (PCBs) Congeners	
			Mean	SD	Mean	SD	Mean	SD
Blue crab	site-wide <sup>b</sup>	24	51	16	59	14	320	100
Carp	RM 7 – RM 17.4	10 <sup>c</sup>	430	420	1,100	620	4,400	2,200
Catfish <sup>d</sup>	RM 4 – RM 17.4	29 <sup>e</sup>	130	100	370	250	2,200	1,600
White perch	site-wide	20	130	70	470	250	2,100	1,100
American eel	site-wide	21	18 <sup>f</sup>	14 <sup>f</sup>	180	110	1,500	1,100
Bass <sup>g</sup>	RM 7 – RM 17.4	6	60	66	280	190	2,400	2,800

<sup>a</sup> Based only on detected concentrations (i.e., all samples in the dataset had detected concentrations), except for American eel and 2,3,7,8-TCDD.

<sup>b</sup> Whole-body concentrations in blue crab collected from RM 0 to RM 10 were used to represent site-wide concentrations (see Section 4.2.5 for a discussion of this uncertainty).

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- c Two carp samples collected between RM 5 and RM 6 were excluded from the calibration dataset because they were collected outside of the modeling area identified for carp (see Section 3.2.5).
- d Includes white and channel catfish.
- e One catfish sample collected near RM 2.2 was excluded from the calibration dataset because it was collected outside of the modeling area identified for catfish (see Section 3.2.5).
- f Summary statistics include one non-detected value in Reach 8 (RM 14 to RM 17.4).
- g Includes smallmouth and largemouth bass.

CB – polychlorinated biphenyl

tetraCB – tetrachlorobiphenyl

RM – river mile

ww – wet weight

TCDF – tetrachlorodibenzo-*p*-dioxin

Exposure concentrations used to calibrate the bioaccumulation model were obtained from the site-specific contaminant fate and transport (CFT) model for the LPRSA. Table 3 provides summary of parameters derived from the CFT model output that were used to calibrate the bioaccumulation model.

**Table 3. Bioaccumulation model parameters derived from CFT model output**

Parameter Name	Model Code	Units	Notes
<b>Chemical-specific parameters</b>			
Chemical concentration in sediment	CST	ng/g dw	top 2 sediment layers layer; area-weighted average
Chemical concentration in porewater	C	ng/g	area-weighted average
Chemical concentration in bioavailable water		ng/g	volume-weighted average
Chemical concentration in water column particulates	CPART	ng/g dw	volume-weighted average
Chemical concentration in near-bottom <sup>a</sup> particulates	CPART_DET	ng/g dw	area-weighted average
<b>Non-chemical-specific parameters</b>			
Mean water temperature	TW	°C	area-weighted average
OC content of sediment	OCSS	fraction	top 2-sediment layer; area-weighted average
OC content of water column particulates	OCPART	fraction	volume-weighted average
OC content of near-bottom particulates <sup>a</sup>	OCPART_DET	fraction	area-weighted average

<sup>a</sup> A total of 10 layers are used to model the water column. Each layer consists of 10% of the water column depth in a given cell. Near-bottom particulates are the particulates in the bottom layer of the water column and are used to represent the chemical concentrations in detritus at the sediment-water column interface.

CFT – contaminant fate and transport

CFT model output was averaged over the calibration period (2011-2013) to develop exposure concentrations for the steady state model (Attachment 2). The average values used in model calibration for each parameter for chemical-specific and non-chemical-specific parameters are presented in Attachment 2.

## 2 DOCUMENTATION OF ASSUMPTIONS REGARDING THE HOME RANGE/EXPOSURE AREA OF THE SPECIES BEING MODELED

USEPA requested information on the justification for spatial extents used for model data comparisons considering the home range of species modeled, and spatial variations in exposure and tissue concentrations.

A modeling (exposure) area was determined for each species/species group included in the model (referred to as a modeling compartment) based on literature information regarding the potential habitat of the various species and site-specific catch information (summarized in Figure 1). The data presented in Figure 1 are based on LPRSA field sampling conducted in 2009 and 2010 (Windward 2011, [in prep]-a) and represent areas where fish were caught. These sampling efforts involved a comprehensive survey of the fish community. The sampling design used to collect fish divided the LPRSA into two-mile segments and dedicated equal sampling time (2 weeks) to each segment. Sampling methods varied with location; specifically electrofishing was used in freshwater, but not in more saline water.

Although fish samples were collected using an unbiased sampling design, in at least some cases the catch for a particular species was distributed unevenly enough across its exposure area to add significant uncertainty about the "correct" exposure concentrations for calibrating. We considered two ways to address this uncertainty. The primary method was to use exposure-area-wide sediment, suspended and near-bottom particulate, and surface and porewater exposure concentrations. This estimation approach emphasizes our understanding of the habitat requirements and exposure areas for the modeled fish populations. The alternative method was to calculate exposure concentrations that were weighted according to where fish were captured, which of course places greater weight on where the fish were caught and relatively less weight on what we know about the habitat requirements and exposure areas for the modeled fish populations.

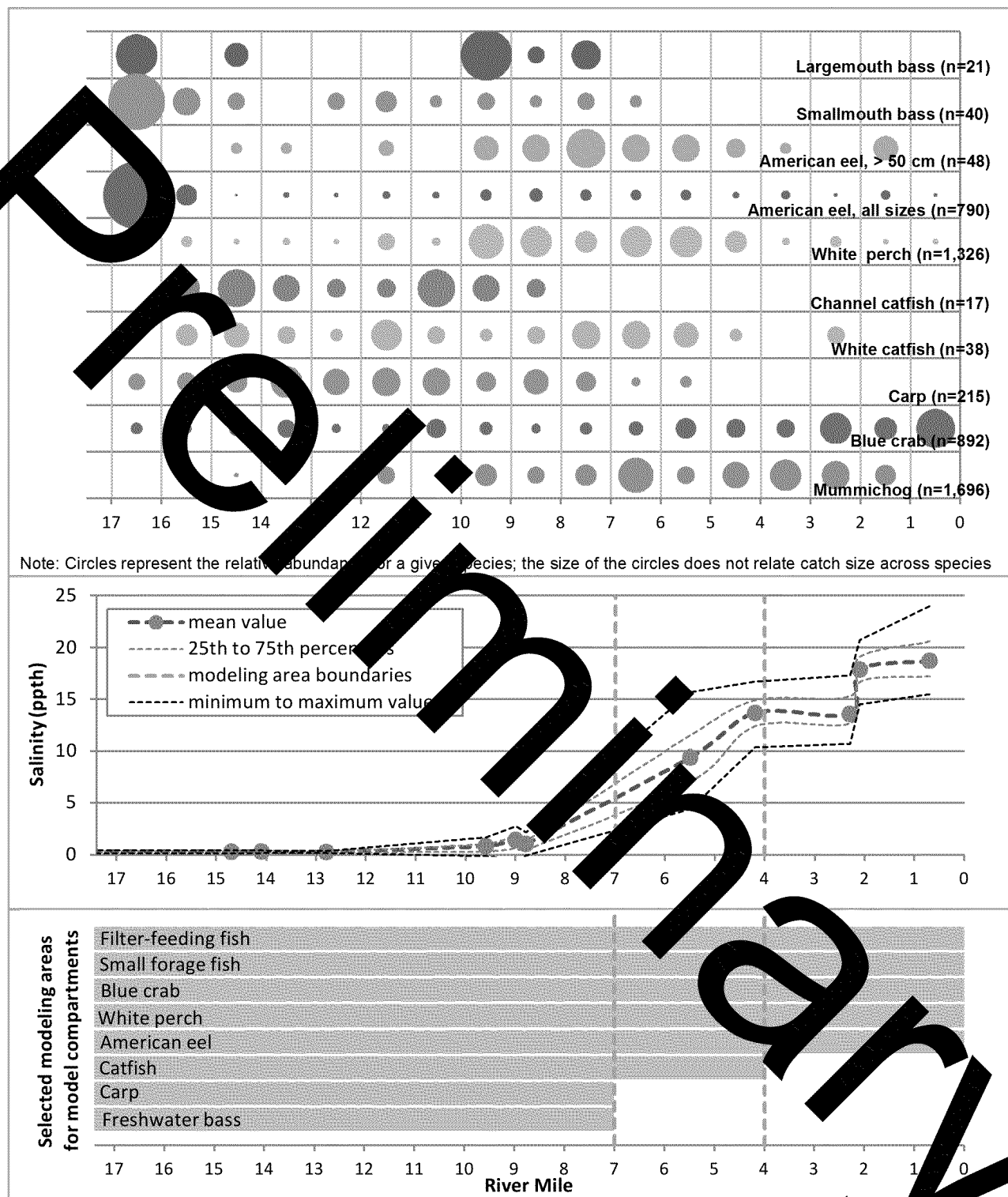
The sensitivity analysis found that predicted tissue concentrations were insensitive to the exposure estimation method (primary or alternative). The calculation for the primary exposure estimation method resulted in tissue concentration predictions that still matched the empirical data well when we used inputs calculated by the alternative exposure estimation method. This sensitivity analysis will be presented in the bioaccumulation model calibration report.

Modeling areas were based on habitat considerations including literature-derived information and site-specific catch distribution data. Human use is another important factor in defining modeling areas. So, for example, it would be inappropriate to model just on reaches of the LPRSA where active remediation would occur because people also fish in other place (and so they should be included in the evaluation). Information regarding the salinity tolerance of the various species was a key line of evidence for determining modeling areas. In the case of small forage fish, water velocity

relative to holding velocity of the fish was another salient factor used to refine the modeling area, as discussed below. The available LPRSA salinity information (Windward [in prep]-c) (as shown on Figure 1) highlights the variability in salinity in lower portions of the LPRSA as a result of the daily tidal cycle. Based on the above information, three modeling areas were identified:

- **RM 1 to RM 17.4 (site-wide)** – The site-wide modeling area was selected for small filter-feeding fish, small forage fish, blue crab, white perch, and American oysters.
- **RM 1 to RM 17.4** – This modeling area was selected for catfish.
- **RM 17 to RM 17.4** – This modeling area was selected for carp and bass.

The selected modeling areas (and corresponding salinity information) are also shown on Figure 1. Table 1 summarizes the catch information and salinity tolerances and provides the rationale for the modeling areas.



**Figure 1. Relative abundance of fish in the LPRSA, salinity data, and selected modeling areas for fish compartments evaluated in the bioaccumulation model**

**Table 4. Fish and crab modeling areas for the LPRSA bioaccumulation model**

Model Compartments	LPRSA Catch Information	Salinity Tolerance	Selected Modeling Area and Rationale for Selection
Small filter-feeding fish	<b>Site-wide</b> – Small filter-feeding fish compartment includes various small fish (e.g., hizzard shad and menhaden) that were caught throughout the LPRSA.	<b>Varies by species</b> – As a group, small filter-feeding fish are present in saltwater, brackish water, and fresh water.	<b>Site-wide</b> – Modeling area is based on catch data (the presence of these species throughout the LPRSA) and the high level of salinity tolerance across species included in this group.
Small forage fish	<b>Site-wide</b> – Small forage fish compartment includes various small benthic fish (e.g., mummichog, shiners, sandfish, and darters) that were caught throughout the LPRSA, primarily on mudflat and shallow water areas.	<b>Varies by species</b> – As a group, small forage fish are present in saltwater, brackish water, and fresh water.	<b>Site-wide (mudflats only)</b> – Modeling area is based on catch data (the presence of these species throughout the LPRSA, primarily on mudflats) and the high level of salinity tolerance across species included in this group.
Blue crab	<b>Site-wide</b> – Blue crab were caught throughout the LPRSA.	<b>High</b> – Blue crab are found in all portions of the estuary, including both high-salinity and low-salinity areas (Hill et al. 1989).	<b>Site-wide</b> – Catch data and salinity information confirm that blue crab use the entire LPRSA.
Carp	<b>Above RM 5</b> – Carp were caught in all areas above RM 5 but were less abundant toward the lower portion of this area (i.e., below RM 7). Catch data indicates that methods used were highly successful in catching carp where present.	<b>Moderate</b> – Carp have a higher salinity tolerance than most freshwater fish (Nico et al. 2014), and can tolerate salinities up to 10 ppt (Lapin et al. 2011), although they prefer lower salinities (2.5 ppt or lower) (NDEP 2001).	<b>RM 7 to RM 17.4</b> – Catch data and available salinity information confirm that although carp might occasionally be found below RM 7, they are primarily present in the freshwater portion of the LPRSA.
Catfish	<b>Above RM 2</b> – The majority of the white catfish caught were collected from RM 4 to RM 16, although only two individuals were caught between RM 2 and RM 3. White catfish were not caught in high numbers in the LPRSA but may be present in areas where they were not caught. Channel catfish were caught from RM 8 to RM 16 but were not caught in high numbers in the LPRSA. They may be present in areas where they were not caught.	<b>Low to moderate</b> – White catfish were reported to be the dominant species in Chesapeake Bay tributaries at salinities up to 12 ppt (Hodall and Schwartz 1983), which demonstrates a moderate salinity tolerance. Channel catfish have a low salinity tolerance and prefer salinities less than 4 ppt (FAO 2014), although they can tolerate moderate salinities (up to 11 ppt) (FAO 2014; McMahon and Terrell 1991; Avault et al. 1969).	<b>RM 4 to RM 17.4</b> – Available salinity and catch data (although limited) indicate that channel catfish are constrained primarily to the freshwater portion of the LPRSA and that white catfish are present in the freshwater and brackish portions of the LPRSA.
White perch	<b>Site-wide</b> – Adult white perch (i.e., individuals > 20 cm in length) were caught throughout the LPRSA.	<b>High</b> – White perch are a semi-anadromous species that is present in saltwater to freshwater habitats.	<b>Site-wide</b> – Catch data and salinity information confirm that white perch use the entire LPRSA.

**Table 4. Fish and crab modeling areas for the LPRSA bioaccumulation model**

Model Compartments	LPRSA Catch Information	Salinity Tolerance	Selected Modeling Area and Rationale for Selection
American eel (> 50 cm)	<b>Site-wide</b> – American eel > 50 cm in length were caught below RM 14; only smaller eel were caught above RM 14. Larger eel (> 50 cm in length) were also caught above Dundee Dam. Catch methods that were successful at catching larger eel could not be used above RM 14 due to sampling limitations.	<b>High</b> – American eel are a catadromous species (i.e., they reproduce in saltwater but mature in fresh/brackish water) and thus are present in fresh, brackish, and coastal waters.	<b>Site-wide</b> – Modeling area is based on the presence of eel throughout the LPRSA (the absence of larger eel above RM 14 does not necessarily indicate that they do not use this portion of the river, particularly because of their presence above Dundee Dam).
Bass	<b>Above RM 6</b> – Both smallmouth and largemouth bass were caught from RM 6 to the Dundee Dam.	<b>Low</b> – Both smallmouth and largemouth bass prefer lower salinities (i.e., < 4 ppt) (Brown et al. 2009; USEPA 2002).	<b>RM 7 to RM 17.4</b> – Catch data and available salinity information confirm that although bass may occasionally use somewhat higher-salinity areas (below RM 7), they are primarily present in the freshwater portion of the LPRSA.

For blue crab and small forage fish, additional discussion of the selected modeling area is presented in the subsections that follow.

## 2.1 Blue crab

Site-wide modeling area was selected for blue crab based on the presence of blue crab throughout the LPRSA during the 2009/2010 sampling efforts (Figure 1) and because of their ability to tolerate a range of salinities. In addition, it is important to note that unlike many invertebrates, adult blue crab (the life stage included in the bioaccumulation model) is highly mobile.

The blue crab has an estuarine-dependent life cycle and moves throughout the estuary based on life stage, gender, and season (Van Engel 1958). After mating, newly hatched blue crab larvae are transported in currents out to sea where they go through several development stages. They return to the estuary and eventually molt into juvenile crab. Small crab spend most of their time in shallow water to avoid predation by adult blue crab and fish and gradually move into deeper water as they grow larger (Hill et al. 1989).

A substantial amount of research has been conducted on the behavior of blue crabs in Chesapeake Bay because blue crab is an important commercial and recreational fishery in the bay. This research is applicable to the Passaic River estuary inasmuch as both are in the mid-Atlantic region with similar climatic conditions. Blue crab are active during the warm, summer months but become inactive and/or depart from much of the estuary during the winter (Hines et al. 1990).

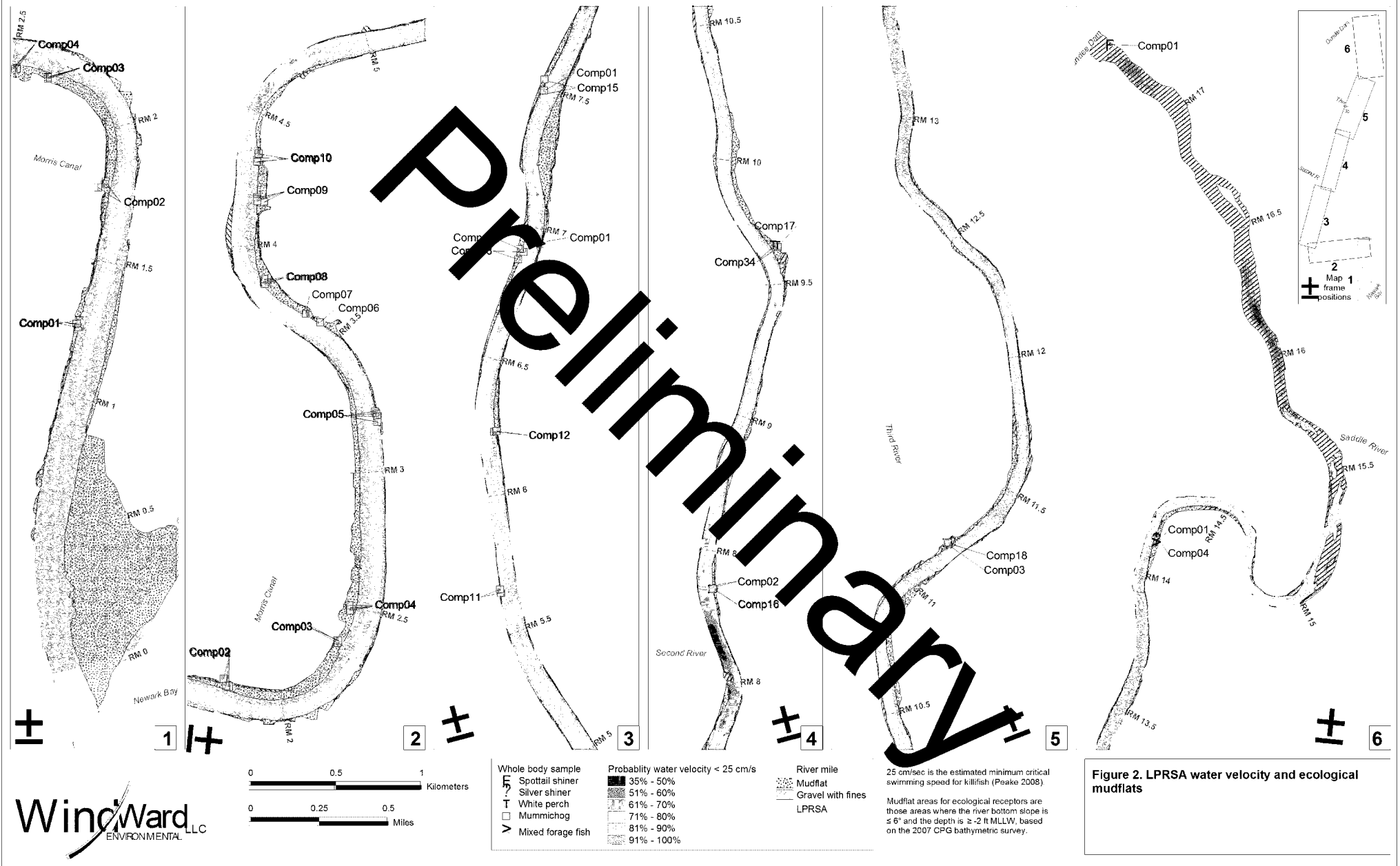
## 2.2 Small Forage Fish

The extent of modeling area for small forage fish such as mummichog was site-wide. The area that is actually used by small forage fish is predominantly restricted to mudflats and shallow areas. These areas provide favorable habitat for small forage fish, which prefer shallow water near the shoreline, tend to inhabit bays and tidally influenced rivers and creeks or estuaries, and typically do not go deeper than 12 ft (3.7 m) (Bigelow and Schroeder 1953). They are usually found within 120 yd (110 m) of shorelines along intertidal marshes and mudflats (Armstrong and Cech 1965 as cited in Abraham 1985; Hardy 1978 as cited in Abraham 1985; Lotrich 1978). Observations made during field efforts conducted in the LPRSA in 2009 and 2011 (Windward 2010, 2011, [in prep]-b) support the habitat information available in literature. Mummichog and other small forage fish were observed in mudflats and shallow-water habitats that often featured overhanging or shoreline vegetation.

LPRSA mudflats were defined as shallow areas ( $\geq -2$  ft mean lower low water) with a gradual ( $\leq 6^\circ$ ) river bottom slope (Figure 2). Most of the mudflat areas identified in Figure 2 feature fine-grained sediment (i.e., silt and sand); however, shallow areas with larger grain sizes (i.e., gravel), primarily in the upper portion of the LPRSA, were

included in the mudflat areas because these shallow areas provide key habitat for some small forage fish such as shiners and darters.

Preliminary



Prepared by lindam 10/27/2014; W:\Projects\06-58-01 Passaic R\lData\GIS\Maps\_and\_Analysis\FoodWebModel\5090\_Water velocity and small forage fish in theLPR\_LSM\_20141027.mxd

During the 2009 and 2010 sampling efforts (Windward 2010, 2011, [in prep]-b), mummichog and banded killifish in the LPRSA were limited to areas with fine-grained sediment; whereas other small forage fish such as shiners and darters were present in shallow areas with larger grain sizes. The presence of mummichog and banded killifish in only fine-grained mudflat areas in the LPRSA is also consistent with velocities that these fish can tolerate. The holding velocity (i.e., the maximum current velocity at which a fish can sustain its position) for mummichog and killifish is reported to be 25 cm/sec (Peake 2008). Areas in which there is a 90% or greater chance of velocities  $\leq$  25 cm/sec are limited to fine-grained mudflats (Figure 1), indicating that the current within the main channel of the LPRSA and above RM 15 would likely preclude the presence of mummichog and killifish. Although average velocities are high in the area above RM 15, other small forage fish species (e.g., shiners and darters) were found along the shoreline in these areas, likely because of the presence of small pockets of quiet water.

Based on this information, the modeling area for small forage fish was defined to include only mudflat areas within the LPRSA. To account for this in the bioaccumulation model, chemical concentrations for the mudflat areas (predicted using the CFT model) were used to estimate exposure for small forage fish and their prey. Thus, bioaccumulation model predicted concentrations in small forage fish prey items were calculated separately using the mudflat area concentrations for small forage fish consumption. Concentrations for the prey items were also calculated based on river-wide (i.e., bank-to-bank) concentrations for consumption by other species.

Though the small forage fish model was calibrated at a site-wide scale, the model was applied at the scale of each of the predator species that consumes small forage fish, i.e., when calibrating the model for species that consume small forage fish, small forage fish tissue chemical concentrations were calculated using model inputs for mudflats in the predators' exposure areas.

Because small forage fish generally have relatively small home ranges (Petrich 1975), the model was also evaluated using a smaller spatial scale for these fish. Co-located sediment data were collected for each of the empirical small forage fish samples, and the model was run using these sediment concentrations (but keeping all other input values the same). Tissue concentrations were predicted within a factor of 2 of all sample locations with two exceptions. The co-located sediment concentrations at the two locations furthest downstream (RM 1.25 and RM 1.77) over-predicted concentrations of 2,3,7,8-TCDD in tissue by a greater margin (factors of approximately 7 and 9). This might be a reflection of the more difficult holding conditions for small forage fish closer to the mouth of the river, meaning that the co-located sediment samples are less reflective of the exposure concentrations for these samples.

Tissue concentrations in small forage fish are highly influenced by chemical concentrations in near-bottom particulates, which were not adjusted as part of this evaluation because co-located data were not available. In addition, even if individual small forage fish have limited home ranges, the prey that they consume are more mobile (i.e., they move with the water currents), meaning that the co-located sediment data are less reflective of the concentrations to which small forage fish are exposed.

Chemical concentrations for all physical media in mudflat areas are shown in Table 5.

Table 5. Chemical-specific concentrations from the CFT model

Parameter by Chemical	Concentration (ng/g)					
	River-Wide			Mudflats Only		
	RM 0 to RM 17.4 (site-wide)	RM 4 to RM 17.4	RM 7 to RM 17.4	RM 0 to RM 17.4 (site-wide)	RM 4 to RM 17.4	RM 7 to RM 17.4
<b>2,3,7,8-TCDD</b>						
Sediment	0.4	0.58	0.64	0.37	0.29	0.29
Suspended particulates	0.2	0.25	0.22	0.19	0.09	0.07
Dissolved contaminants <sup>a</sup>	$2.5 \times 10^{-7}$	$2.4 \times 10^{-7}$	$1.9 \times 10^{-7}$	$1.9 \times 10^{-7}$	$7.0 \times 10^{-8}$	$5.3 \times 10^{-8}$
Porewater	$5 \times 10^{-6}$	$6.5 \times 10^{-6}$	$7.4 \times 10^{-6}$	$2.9 \times 10^{-6}$	$3.1 \times 10^{-6}$	$3.1 \times 10^{-6}$
Near-bottom particulates	0.2	0.26	0.22	0.20	0.099	0.07
<b>TetraCB</b>						
Sediment	232	229	217	232	198	190
Suspended particulates	216	237	234	228	181	169
Dissolved contaminants <sup>a</sup>	$6.0 \times 10^{-4}$	$5.8 \times 10^{-4}$	$5.4 \times 10^{-4}$	$6.1 \times 10^{-4}$	$5.7 \times 10^{-4}$	$5.6 \times 10^{-4}$
Porewater	$2.4 \times 10^{-3}$	$3.0 \times 10^{-3}$	$2 \times 10^{-3}$	$2.4 \times 10^{-3}$	$3.4 \times 10^{-3}$	$3.4 \times 10^{-3}$
Near-bottom particulates	213	240	237	250	186	172

Note: CFT model output is from October 31, 2014 (with updates provided on January 14 and March 2, 2015). Output from the CFT model was averaged over the 3-year calibration period for use in the calibration of the bioaccumulation model (see Attachment 1 for details).

<sup>a</sup> Estimates of the concentrations of dissolved contaminants in water were provided as part of the CFT model output. Thus, equations in Arnot and Gobas (2004) were not needed to estimate this parameter from empirical or estimated total water concentrations.

CFT – contaminant fate and transport

RM – river mile

TCDD – tetrachlorodibenzo-*p*-dioxin

tetraCB – tetrachlorobiphenyl

### 3 CHOICES FOR MODEL-TO-DATA COMPARISON TO ASSESS CALIBRATION

USEPA requested information on the species used for calibration and consistency of the temporal and spatial extents of the tissue data and exposure concentrations.

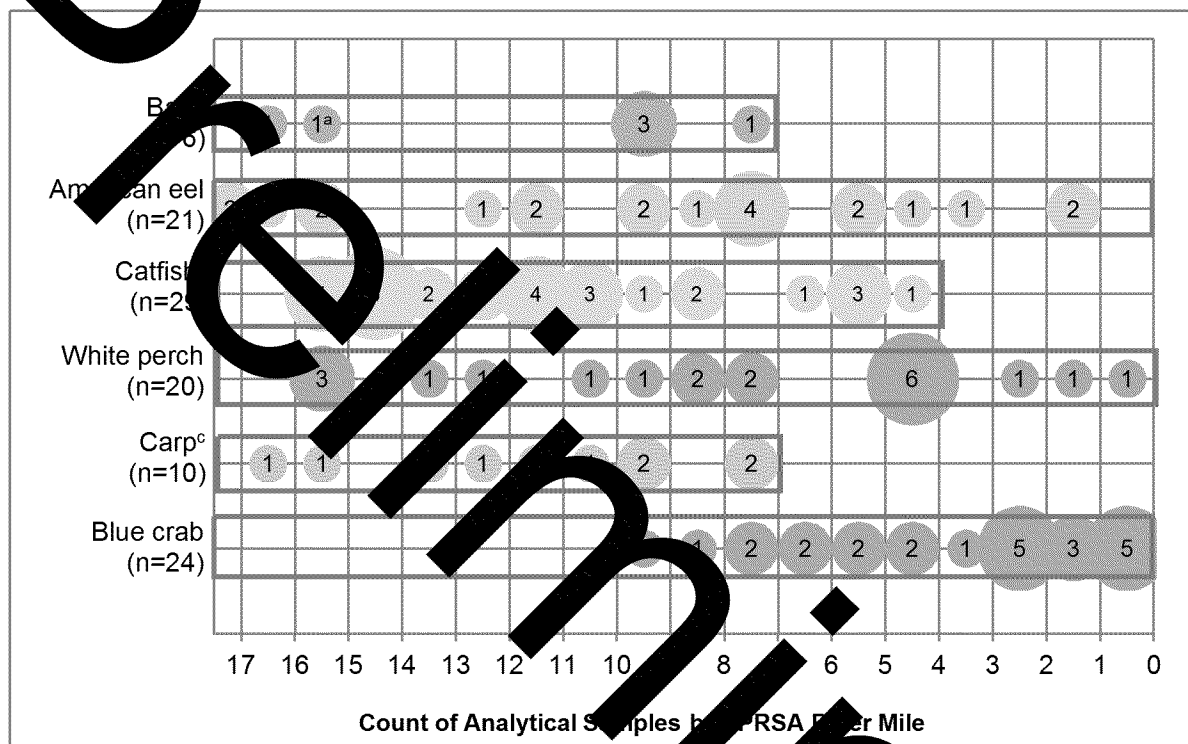
Six target species were used to calibrate the bioaccumulation model: blue crab, carp, catfish, white perch, American eel, and bass. The following factors were considered when evaluating the representativeness of the empirical tissue data: spatial coverage of the samples, number of available samples, and sample type (individual vs. composite). Empirical tissue data were not evaluated on a temporal basis because all data are from same time period. Details on and the rationale for the empirical tissue data used in model calibration are provided in Attachment 1 and summarized below.

LPRSA tissue data included in the calibration dataset were collected and analyzed as part of 2009 EPC tissue sampling event, which was designed for the purpose of developing a comprehensive tissue sample database for the LPRSA, and thus the dataset is considered to be generally representative of the species and concentrations present in the LPRSA.

To evaluate the spatial coverage of the available analytical data, Figure 3 presents a summary of the number (by river mile) of analytical samples available for each species in the calibration dataset, and indicates the modeling area selected for each species. As can be seen in this figure, the analytical samples for each species in the calibration dataset are generally distributed throughout the associated modeling area, and consist of 10 or more samples. The exceptions to this include the following:

- **Bass** – Only six bass samples were analyzed to cover the approximately 10-mile modeling area. Sample average tissue concentration can be considered representative of the bass modeling area because the samples were collected using an unbiased sampling design, but the smaller number and uneven spatial distribution of the bass collected suggests that the sample average is more uncertain than the sample average for other species with large sample sizes. Higher variability in sediment surface-weighted average concentrations (SWACs) for 2,3,7,8-TCDD also contribute to uncertainty about average bass concentration because of the possibility that subsets (of unknown size) of the LPRSA bass population would occupy unique reaches with significantly different SWACs.
- **Blue crab** – The dataset includes 24 whole-body samples (calculated as the re-constituted samples from the muscle/hepatopancreas and carcass samples). As stipulated by USEPA, only muscle/hepatopancreas from blue crab samples collected from above RM 10 was analyzed for tissue chemistry. Therefore, no carcass tissue concentration data were available to calculate re-constituted whole body tissue chemical concentrations for blue crab samples collected above RM 10. The muscle/hepatopancreas samples (available from throughout the

LPSRA, including above RM 10) were evaluated to determine if the absence of whole-body data above RM 10 was likely to impact the calibration of the bioaccumulation model based on the available whole-body data. This is discussed in further detail below in the subsection on the blue crab whole-body tissue dataset.



Note: Gray outlined boxes indicate the modeling area for each species. Refer to Table 1 for information regarding whether samples represent individual or composite samples.

- <sup>a</sup> This bass composite sample contained two individuals from RM 15 to RM 16, and one from RM 16 to RM 17; this composite sample is shown as being collected from RM 15 to RM 16.
- <sup>b</sup> One individual catfish sample was excluded from the calibration dataset because it was collected outside of the modeling area identified for catfish (see Section 3.2.5). This sample was collected from near RM 12.2.
- <sup>c</sup> Two individual carp samples were excluded from the calibration dataset because they were collected outside of the modeling area identified for carp (see Section 3.2.5). These samples were collected from near RM 5 and RM 6.

**Figure 3. Number of analytical samples by LPSRA river mile for the calibration dataset**

Additional topics related to the calibration dataset are discussed in the following subsections.

### ***American Eel as a Single Size Class***

For the purposes of model calibration and parameterization, all whole-body eel data were included in the calibration dataset as a single class size. Table 6 presents a

comparison of average concentrations for three different groups of eel: all eel, eel > 50 cm in length, and eel > 40 cm in length. Although concentrations vary somewhat depending on the size class, they are not sufficiently different to significantly affect model calibration. The tissue concentrations are affected by the absence of larger eel in the upper river miles where concentrations in sediment were generally lower. Concentrations in whole-body eel data in the upper portion of the LPRSA (i.e., from RM 12 to the Dundee Dam) are lower than those in the rest of the LPRSA (see Attachment 1). Overall, concentrations do not appear to be influenced by eel lengths or weights.

**Table 6 Comparison of empirical eel data**

Eel size Group <sup>a</sup>	Number of Samples	Area Covered in the LPRSA	Average Concentration (µg/kg ww)		
			2,3,7,8-TCDD	TetraCB	Total PCBs
All eel	21	site-wide	0.018 <sup>b</sup>	180	1,500
Eel > 40 cm	13	below RM 12	0.024	220	1,900
Eel > 50 cm		below RM 10	0.026	230	1,700

<sup>a</sup> For composite samples, the size for a given sample was determined by the size of the largest eel in the composite.

<sup>b</sup> Average includes one non-detected value in sample near RM 16.

PCB – polychlorinated biphenyl

tetraCB – tetrachlorobiphenyl

RM – river mile

ww – wet weight

TCDD – tetrachlorodibenzo-*p*-dioxin

### **Blue Crab Whole-Body Tissue Dataset**

Due to the lack of carcass tissue chemistry data for calculating whole-body tissue concentrations above RM 10, the whole-body data (calculated from the re-constituted samples from the muscle/hepatopancreas and carcass samples collected from RM 0 to RM 10) were used to represent the site-wide average whole-body chemical concentrations in blue crab for the purpose of calibrating the bioaccumulation model. To address this possible uncertainty, chemical concentrations in muscle-hepatopancreas tissue samples (which were available from throughout the LPRSA) were compared (Table 7). The site-wide muscle/hepatopancreas tissue 2,3,7,8-TCDD and tetraCB concentrations were approximately 20% lower than from RM 0 to RM 10 concentrations, so the model might contain a small bias to overestimate chemical concentrations in whole-body crab tissue.

**Table 7. Comparison of LPRSA blue crab muscle/hepatopancreas concentrations**

LPRSA Area	No. of Samples	Muscle/Hepatopancreas Concentration					
		2,3,7,8-TCDD (ng/kg ww)		TetraCB (µg/kg ww)		Total PCBs (µg/kg ww)	
		Range	Average	Range	Average	Range	Average
RM 0 to RM 10 (Reaches 1 to 5) <sup>a</sup>	24	24 – 110	61	23 – 94	69	130 – 790	370
RM 10 to RM 17.4 (Reaches 6 to 8)	17	4 – 71	33	13 – 62	39	76 – 410	260
RM 0 to RM 17.4 (Reaches 1 to 8)	41	4 – 110	49	13 – 94	57	76 – 790	330

Note: Additional information is available in Attachment 1.

<sup>a</sup> Recalculated whole-body data based on muscle/hepatopancreas and carcass samples from this LPRSA area (RM 0 to RM 10) used to represent site-wide concentrations in the model calibration. No carcass data were analyzed based on blue crab collected from above RM 10.

LPRSA – Lower Passaic River Study Area

na – not applicable

PCB – polychlorinated biphenyl

RM – river mile

TCDD – tetrachlorodibenzo-*p*-dioxin

tetraCB – tetrachlorobiphenyl

ww – wet weight

#### 4 DOCUMENTATION OF THE $K_{ow}$ AND $D_w$ VALUES USED IN THE MODEL

USEPA requested information on the  $K_{oc}$ ,  $K_{ow}$  and  $D_w$  values used in the model. It is not clear what USEPA intended for  $D_w$  to represent; there is no parameter  $D_w$  in the bioaccumulation model. Chemical-specific  $K_{ow}$  distributions, log  $K_{ow}$  values, and rationale/sources for the selected values are presented in Table 8.  $K_{oc}$  was not used in the bioaccumulation model.

**Table 8. Chemical-specific  $K_{ow}$  distributions**

Chemical	Distribution <sup>a</sup>	Log $K_{ow}$ Value		Rationale/Source
		Preliminary Calibrated Value <sup>b</sup>	Calibrated Value	
2,3,7,8-TCDD	type: triangular nominal value: 6.38 range: 5.38 – 8.93	6.81	6.81	<b>Nominal value</b> – EPA RAIS (2009) <b>Range</b> – <i>Handbook of Basic Chemical Properties and Environmental Fate for Organic Chemicals</i> (Macdonald et al. 2006)
TetraCB	type: triangular nominal value: 6.00 range: 5.38 – 6.65	5.85	5.90	<b>Nominal value</b> – CAP model (MetroQua 2007), which cited Hawker and Connell (1988) as the source of $K_{ow}$ values for PCB homologues <b>Range</b> – Maximum and minimum values for individual congeners within a homologue group (Hawker and Connell 1988)

<sup>a</sup> The term “nominal value” refers to a reasonable best estimate based on literature information prior to considering site-specific model calibration data. For parameters that were assigned triangular distributions, the nominal value was used as the mode.

<sup>b</sup> Values from the December 18, 2013, preliminary calibration of the bioaccumulation model for the LPRSA were used as the starting point for model calibration.

CARP – Contamination Assessment and Reduction Project

K<sub>ow</sub> – octanol-water partition coefficient

LPRSA – Lower Passaic River Study Area

PCB – polychlorinated biphenyl

SPARC – Scholarly Publishing & Academic  
Resources Coalition

TCDD – tetrachlorodibenzo-*p*-dioxin

tetraCB – tetrachlorobiphenyl

## **BASIS FOR REPORTED PARAMETER-CALIBRATION RANGES FOR INVERTEBRATE DIETARY ASSIMILATION EFFICIENCIES**

USEPA requested information on the parameter-calibration ranges for invertebrate dietary assimilation efficiencies used in the bioaccumulation model.

Dietary absorption efficiencies for invertebrates for lipid, non-lipid organic carbon (NLOC), and non-lipid organic matter (NLOM) are parameters to which the model was determined to be sensitive during calibration. As part of calibration different dietary absorption efficiency assumptions were considered before selecting a final calibrated value. A single value was selected for all nine dietary absorption efficiencies (i.e., lipid, NLOC, and NLOM for each of the three benthic invertebrate compartments in the bioaccumulation model) because there is insufficient evidence to warrant using distinct values for the different efficiencies. A calibrated dietary absorption efficiency of 0.40 was selected (see Table 9 for summary of parameter distributions and rationale).

**Table 9. Invertebrate adsorption efficiencies parameter distributions and rationale**

Parameter by Model Compartment	Units	Modeling Area	Nominal Value	Distribution Type	Distribution Value <sup>a</sup>	Calibrated Value	Source Notes
<b>Invertebrate Adsorption Efficiencies (for invertebrates and blue crab)</b>							
Dietary AE of lipid	none		0.75	triangle	mode = 0.75 min = 0.15 max = 0.96	0.40	Data from Roditi and Fisher (1999), Berge and Brevik (1996), Gordon (1966), and Parkerton (1993), as cited in Arnot and Gobas (2004); studies involved zebra mussels from tidal freshwater section of the Hudson River and polychaetes from Cape Cod intertidal flats
Dietary AE of NLOM	none	site-wide	0.75	triangle	mode = 0.75 min = 0.15 max = 0.96	0.40	Data from Roditi and Fisher (1999), Berge and Brevik (1996), Gordon (1966), and Parkerton (1993), as cited in Arnot and Gobas (2004); studies involved zebra mussels from the tidal freshwater section of the Hudson River and polychaetes from Cape Cod intertidal flats
Dietary AE of NLOC	none	site-wide	0.40	triangle	mode = 0.75 min = 0.15 max = 0.96	0.40	Windward contacted Frank Gobas to discuss whether dietary AEs of NLOM and NLOC for invertebrates of 0.4 are reasonable estimates. Gobas indicated that invertebrate dietary adsorption efficiencies are expected to be lower than those for fish (particularly pelagic fish) (Gobas 2014). The dietary NLOM and NLOC adsorption efficiencies for fish were estimated to be in the range 0.50 to 0.65 based on rainbow trout tetraCB data from Nichols et al. (2001), as cited in Arnot and Gobas (2004), so 0.4 was determined to be a reasonable calibrated value. It falls near the center of the range developed based on the available invertebrate data and is consistent with the expectation that the value is somewhat lower for invertebrates than for fish.
Dietary AE of water	none	site-wide	0.55	point	na	0.55	Value from Gobas and Arnot (2005)

AE – assimilation efficiency  
NLOC – non-lipid organic carbon  
NLOM – non-lipid organic matter

## 6 BASIS FOR REPORTED PARAMETER-CALIBRATION RANGES FOR 2,3,7,8-TCDD METABOLIC BIOTRANSFORMATION RATES

USEPA requested information on the parameter-calibration ranges for 2,3,7,8-TCDD metabolic biotransformation rates used in the bioaccumulation model. Metabolic biotransformation rate constants ( $K_M$ s) were used in the model for 2,3,7,8-TCDD, for small benthic invertebrates, blue crab, and fish (summarized in Table 10). The selection of the species-chemical combinations for which  $K_M$  values were applied is discussed in greater detail in Attachment 3.

**Table 10. 2,3,7,8-TCDD metabolic biotransformation rate constants**

Model Compartment by Chemical	Selected $K_M$ (fraction/day)		Rationale <sup>a</sup>
	$K_M$ Distribution	Calibrated Value	
Benthic invertebrates and blue crab	type: uniform <sup>b</sup> nominal value: 0.013 range: 0.007 – 0.024	0.018	CYP450 1A expression (CYP450 1A1 is the most important enzyme in TCDD metabolism for vertebrates) is not known to occur in benthic invertebrates. It is possible that benthic invertebrates metabolize 2,3,7,8-TCDD by a different route than vertebrates. Alternatively, it might be that $K_M$ serves as a surrogate rate constant for some other process(es) reducing 2,3,7,8-TCDD uptake or increasing loss by benthic invertebrates. Work performed for CARP for the New York/New Jersey Harbor estuary (HydroQual 2007) found that worms have approximately 10 times lower than BSAFs for PCBs with similar $K_M$ s. The HydroQual (2007) report stated that “this suggests that either there is an inefficient transfer of dioxin/furan congeners from sediment, or that worms also possess the capacity to metabolize dioxin and furan congeners.” No invertebrate-specific rates are available, and thus the distribution for fish was also applied to invertebrates.
Carp	type: uniform <sup>b</sup> nominal value: 0.014 range: 0.0016 – 0.056	0.0065	Species-specific data on metabolic biotransformation rates are available for carp and provide evidence that the $K_M$ values for carp are lower than for other fish Arnot et al. (2008a); (Arnot et al. 2008b), so carp metabolic biotransformation rates were calibrated separately from other fish using carp-specific values.
American eel	type: uniform <sup>b</sup> nominal value: 0.04 range: 0.0016 – 0.082	0.075	Available literature and LPRSA empirical data indicate that the bioaccumulation pattern for eel is different than that for other fish. In a study of European eel (a single species), van der Oost et al. (1996) concluded that the low bioaccumulation of dioxins/furans was most likely due to reduced uptake, effective metabolic clearance, or both. No eel-specific metabolic biotransformation rate data were available, and thus high end estimates (i.e., the 97.5 <sup>th</sup> percentile estimates of $K_M$ ) of metabolic biotransformation rates were derived using fish data from Arnot et al. (2008a). The $K_M$ could represent a very high metabolic biotransformation rate, or it could represent a surrogate for describing another process that results in reduced uptake relative to other fish.
Other fish <sup>c</sup>	type: uniform <sup>b</sup> nominal value: 0.013 range: 0.007 – 0.024	0.018	Metabolic biotransformation rates were developed using all available metabolic biotransformation rates for 2,3,7,8-TCDD (i.e., rates for all available species) from Arnot et al. (2008a).

BSAF – biota-sediment accumulation factor

CARP – Contaminant Assessment and Reduction Project

$K_M$  – metabolism biotransformation rate constant

LPRSA – Lower Passaic River Study Area

PCB – polychlorinated biphenyl

TCDD – tetrachlorodibenzo-*p*-dioxin

## SOURCES OR DATA ANALYSIS BEHIND FOOD WEB COMPOSITION AND DIETARY PREFERENCES FOR EACH SPECIES

USEPA requested information on the sources or data analysis behind food web composition and dietary preferences for each species used in the bioaccumulation model. The scale and source of species-specific diet data are detailed in Table 11. Diets were assigned based on a review of regional and general scientific literature. Life history profiles, included as Attachment 2 of the revised risk analysis and risk characterization CARC plan (Windward and AECOM [in prep]), presented general data from the literature regarding the life histories and potential diets of LPRSA ecological receptors. Attachment 4 presents the details of the development of those dietary assumptions (i.e., the dietary items included and the portions of each prey item).

**Table 11. Parameter distributions and rationale for the selection of species-specific diets**

Prey Items by Model Compartment	Distribution Type	Nominal Value (%)	Range (%)	Calibrated Value (%)	Rationale and Source <sup>b</sup>
<b>Zooplankton</b>					
Phytoplankton/algae	point est.	100	na	100	<b>General</b> – It was assumed that the portion of carnivorous zooplankton in the LPRSA as compared with the portion of planktivores is negligible.
<b>Benthic Invertebrate DEPs<sup>c</sup></b>					
Sediment solids	point est.	na	na	100	<b>General</b> – DEPs consume primarily sediment solids. <b>Sediment</b> – Sediment solids were assumed to constitute the entire diet of deposit feeders. Organic detritus (which includes dead and decaying algae/plankton) is not expected to be a major component of the sediment ingested by DEPs since these organisms typically feed vertically (i.e., head-down).
Particulates/detritus (near-bottom)	point est.	na	na	na	
<b>Benthic Invertebrate DETs<sup>d</sup></b>					
Sediment solids	point est.	0	na	0	<b>General</b> – DETs (including benthic filter feeders) eat organic particulate material at the sediment surface or from the water column. Some phytoplankton/algae and zooplankton are also likely to be consumed, inasmuch as this model compartment also includes small omnivores that will consume some plant or animal matter, if available, in addition to detritus.
Particulates/detritus (near-bottom)	uniform	70	60 – 90	70	
Phytoplankton/algae	uniform	15	5 – 20	15	<b>Sediment</b> – Based on DET feeding habits, particulates/detritus on the river bottom (which includes dead and decaying plankton and plant material) is assumed to constitute the majority of the diet.
Zooplankton	uniform	15	5 – 20	15	
<b>Benthic Invertebrate C/Os<sup>e</sup></b>					
Sediment solids	point est.	0	na	0	<b>General</b> – C/Os eat only small benthic organisms, dead organisms, plankton, and algae. The majority of their diet is expected to be composed of benthic invertebrates.
Particulates/detritus (near-bottom)	uniform	2	0 – 5	2	
Phytoplankton/algae	uniform	12	10 – 15	12	<b>Sediment</b> – Sediment and particulates/detritus are not anticipated to be a significant component of the C/O diet, although some minor particulate/detritus ingestion is possible given their feeding habits.
Zooplankton	uniform	12	10 – 15	12	
Benthic invertebrates	uniform	74	60 – 85	74	<b>Benthic invertebrates</b> – C/Os are assumed to consume primarily DETs. Based on the feeding habits of C/Os (i.e., foraging in sediment for food), the consumption of a smaller amount of DEPs could also occur.
DEPs <sup>f</sup>	uniform	10	0 – 20	10	
DETs <sup>g</sup>	uniform	90	80 – 100	90	

**Table 11. Parameter distributions and rationale for the selection of species-specific diets**

Prey Items by Model Compartment	Distribution Type	Nominal Value (%)	Range (%)	Calibrated Value (%)	Rationale and Source <sup>b</sup>
<b>Filter-Feeding Fish<sup>g</sup></b>					
Sediment solids	point estimate	0	na	0	<b>General</b> – The diet for filter-feeding fish is based on that of Atlantic menhaden, which are opportunistic filter feeders as juveniles and adults, consuming zooplankton, phytoplankton, and diatom chains depending on the availability of prey items. The majority of prey is identified as “amorphous material” and is represented by particulates/detritus. If phytoplankton abundance is limited, menhaden may consume more detritus. In addition, the portion of zooplankton decreases as fish move from open waters to marshes (Rogers and van den Avyle 1989; Jeffries 1975). Thus particulates/detritus (from the water column) were estimated to be half of their diet, with phytoplankton/algae and zooplankton making up the remainder of the diet based on general portion estimates provided by FishBase (2014). <b>Sediment</b> – Sediment solids are not expected to be ingested by filter feeders.
Particulates/detritus (water column)	uniform	50	40 – 60	50	
Phytoplankton/algae	uniform	25	10 – 40	25	
Zooplankton	uniform	25	10 – 30	25	
<b>Small Forage Fish<sup>h</sup></b>					
Sediment solids	uniform	1	0 – 3	1	<b>General</b> – The diet for small forage fish is based on mummichog, which feed primarily on small crustaceans (i.e., amphipods, tanaids, copepods, and ostracods), polychaetes, insects (adult and larval), detritus, and algae (Abraham 1985; Allen et al. 1994; James-Pirri et al. 2001; Kneib 1986; Smith et al. 2003). Benthic invertebrates are assumed to comprise the majority of the diet, with detritus, algae, and zooplankton each making up a smaller portion of the diet; actual dietary portions are likely a factor of availability in the LPRSA. <b>Sediment</b> – Studies have reported the presence of detritus in mummichog stomachs but did not report the specific composition of sediment (see Attachment 4). However mummichog longer than 2.5 cm was present in the LPRSA, consume some near-bottom detritus and likely incidentally ingest small portion of sediment solids while feeding. <b>Benthic invertebrates</b> – Small forage fish are assumed to consume small benthic invertebrates proportional to the relative biomass of benthic invertebrates in the LPRSA. The numbers represent the relative biomass for the small forage fish modeling area (site-wide). LPRSA benthic invertebrate biomass may vary across seasonal and annual abundance and conditions.
Particulates/detritus (near-bottom)	uniform	15	0 – 30	15	
Phytoplankton/algae	uniform	15	0 – 30	15	
Zooplankton	uniform	4	0 – 5	4	
Benthic invertebrates	uniform	65	20 – 100	65	
DEPs <sup>i</sup>	uniform	9 <sup>j</sup>	0 – 50	9	
DETs <sup>j</sup>	uniform	85 <sup>j</sup>	50 – 100	85	
C/Os <sup>k</sup>	uniform	6 <sup>j</sup>	0 – 50	6	
<b>Blue Crab</b>					
Sediment solids	uniform	2	0 – 5	2	<b>General</b> – Blue crab are opportunistic feeders whose diet varies depending on their size and prey availability. The blue crab diet consists primarily of mollusks and crustaceans (including other blue crab); small fish make up a smaller portion of the diet. The dietary portions were primarily based on a Chesapeake Bay estuary study of blue crabs averaging 13 cm in width (Hines et al. 1990), and qualitatively on studies from northern Florida (Laughlin 1982) and Raritan Bay (Stehlik et al. 1998), as described in Attachment 4. <b>Sediment</b> – The ingestion of sediment, particulates, and/or detritus was reported to be a minimal component of the blue crab diet in the available literature studies (Laughlin 1982; Stehlik et al. 1998; Hines et al. 1990). <b>Benthic invertebrates</b> – Blue crab are assumed to consume small benthic invertebrates
Particulates/detritus (near-bottom)	uniform	1	0 – 5	1	
Benthic invertebrates	uniform	83	60 – 90	83	
DEPs <sup>i</sup>	uniform	9 <sup>j</sup>	0 – 50	9	
DETs <sup>j</sup>	uniform	85 <sup>j</sup>	50 – 100	85	
C/Os <sup>k</sup>	uniform	6 <sup>j</sup>	0 – 50	6	
Small fish	uniform	14	5 – 25	14	

**Table 11. Parameter distributions and rationale for the selection of species-specific diets**

Prey Items by Model Compartment	Distribution Type	Nominal Value (%)	Range (%)	Calibrated Value (%)	Rationale and Source <sup>b</sup>
Filter-feeding fish <sup>i</sup>	point est.		na	25	proportional to the relative biomass of benthic invertebrates in the LPRSA. The numbers represent the relative biomass for the blue crab modeling area (site-wide). LPRSA benthic invertebrate biomass may vary across seasonal and annual abundance and conditions. <b>Small fish</b> – Blue crab are primarily bottom feeders, and thus the fish portion of their diet is assumed to be composed primarily of benthic small forage fish.
Small forage fish <sup>i</sup>	point est.	75	na	75	
<b>Common Carp</b>					
Sediment solids	uniform		0 – 25	15	<b>General</b> – Carp are highly opportunistic feeders and have a variable diet. Detritus, algae, plants, and small benthic invertebrates make up the majority of the carp diet; carp may also consume insects, small fish, and plankton (Maryland DNR 2007; Garcia-Berthou 2001; USGS 2010; Walburg and Nelson 1966). Benthic invertebrates are expected to comprise the greatest portion of the carp diet.
Particulates/detritus (near-bottom)	uniform		10 – 50	30	
Phytoplankton/algae	uniform	5	0 – 10	5	<b>Sediment</b> – Studies have reported the presence of detritus in carp stomachs (indicating some incidental ingestion of sediment) but did not quantify sediment consumption (Campos 2005; Walburg and Nelson 1966). Based on their feeding habits, sediment solids and particulates/detritus are anticipated to be an important component of the carp diet.
Benthic invertebrates	uniform	54	25 – 100	50	
DEPs <sup>i</sup>	uniform	14 <sup>i</sup>	0 – 50	14	<b>Benthic invertebrates</b> – Carp are assumed to consume small benthic invertebrates proportional to the relative biomass of benthic invertebrates in the LPRSA. The numbers represent the relative biomass for the carp modeling area (RM 4 to 17.4). LPRSA benthic invertebrate biomass may vary across seasonal and annual abundance and conditions.
DETs <sup>i</sup>	uniform	75 <sup>i</sup>	50 – 100	75	
C/Os <sup>i</sup>	uniform	11 <sup>i</sup>	0 – 50	11	<b>Small fish</b> – Carp are primarily bottom feeders, and thus the fish portion of their diet is assumed to be composed entirely of benthic small forage fish.
Small fish	uniform	1	0 – 5		
Filter-feeding fish <sup>i</sup>	point est.	0	na	0	
Small forage fish <sup>i</sup>	point est.	100	na	100	

**Table 11. Parameter distributions and rationale for the selection of species-specific diets**

Prey Items by Model Compartment	Distribution Type	Nominal Value (%)	Range (%)	Calibrated Value (%)	Rationale and Source <sup>b</sup>
<b>Catfish (white and channel)</b>					
Sediment solids	uniform	5	0 – 10	5	<p><b>General</b> – Both channel and white catfish are opportunistic feeders that will feed on all available prey items. Adult white catfish are carnivorous bottom feeders, preying on larger invertebrates and fish (California Fish Website 2013b). Common dietary items for adult white catfish include invertebrates (e.g., amphipods, crayfish, shrimp, and small clams), small fish, and detritus, with small fish and benthic invertebrates comprising the majority of the adult diet by volume (Turner 1966b; FishBase 2014). Adult channel catfish have been found to prey primarily on insects, detritus, crayfish, and small fish (NJDEP 2001b; Wellborn 1988; California Fish Website 2013a). A study conducted in the Susquehanna River (a system that is less urbanized than the LPRSA) found that channel catfish consumed primarily small fish and plants (generally intermingled with invertebrates, suggesting incidental ingestion), which made up 43 and 45% of the diet, respectively, with the remainder of the diet being composed of mollusks, insects, crustaceans, and inorganic matter (Fewless 1980). Channel catfish from Washington and California rivers consumed 26 to 65% benthic invertebrates and 25 to 73% small fish, as well as a small proportion of insects and mammals (FishBase 2014). The percentage of the channel catfish diet consisting of fish was reported to be as high as 75% in “natural waters” (Wellborn 1988), although this is unlikely in a highly urbanized system such as the LPRSA. Phytoplankton/algae consumption in the LPRSA is assumed to be minimal due to its limited presence relative to other available prey items.</p> <p><b>Sediment</b> – A small portion of sediment solids and particulate/detritus ingestion was included based on the benthic foraging behavior of catfish species.</p> <p><b>Benthic invertebrates</b> – Major benthic invertebrate prey for white and channel catfish include C/Os (i.e., crayfish, clams, shrimp, snails, and mollusks) and DETs (i.e., clams, shrimp, snails and amphipods). These were assumed to represent equal portions of their benthic diet based on their feeding habits and information regarding their preferred invertebrate prey types (Attachment 4).</p> <p><b>Small fish</b> – Catfish are primarily benthic feeders; thus, the fish portion of their diet is composed mostly of benthic small forage fish. However, some portion of pelagic fish may be preyed upon by catfish, inasmuch as both white and channel catfish are known to swim in the water column to feed on pelagic fish such as gizzard shad (California Fish Website 2013b; Wellborn 1988; FishBase 2014).</p>
Particulates/detritus (near-bottom)	uniform	5	5 – 20	10	
Phytoplankton/algae	uniform	2	0 – 5	2	
Benthic invertebrates	uniform	43	20 – 60	40	
DEPs <sup>f</sup>	point est.	0	na	0	
DET <sup>f</sup>	uniform	50	0 – 100	50	
C/Os <sup>f</sup>	uniform	50	0 – 100	50	
Small fish	uniform	40	20 – 60	40	
Filter-feeding fish <sup>l</sup>	uniform	25	0 – 50	25	
Small forage fish <sup>l</sup>	uniform	75	50 – 100	75	

**Table 11. Parameter distributions and rationale for the selection of species-specific diets**

Prey Items by Model Compartment	Distribution Type	Nominal Value (%)	Range (%)	Calibrated Value (%)	Rationale and Source <sup>b</sup>
<b>White Perch (mature)</b>					
Sediment solids	point estimate	0	na	0	<p><b>General</b> – Amphipods, shrimp, and copepods were common white perch dietary components in regional studies on the Hudson and Hackensack Rivers (Bath and O'Connor 1985; Weis 2005). Depending on the season and the fish size, white perch from the Great Lakes have been found to consume large portions of small fish (Schaeffer and Margraf 1986); and perch in the York River (Virginia) feed heavily on crab (McGrath 2005). However, regional studies (i.e., on the Hudson and Hackensack Rivers) did not report much consumption of crab or fish by white perch (Bath and O'Connor 1985; Weis 2005; TAMS 1999). Regional data were used to develop dietary proportions, using data from studies in New Jersey and New York, which indicated that the majority of the perch diet is composed of benthic invertebrates, followed by a small portion of small fish. The diet selected for the LPRSA also accounts for the consumption of small amounts of detritus, phytoplankton, and zooplankton based on information from other studies that have indicated that perch may consume small amounts of these items when they are available and/or incidentally while feeding (McGrath 2005; Schaeffer and Margraf 1986; Bath and O'Connor 1985; Weis 2005; Weisberg and Janicki 1990). The selected ranges are intended to reflect opportunistic foraging habits of white perch.</p> <p><b>Sediment</b> – Studies did not report the specific consumption of sediment; a small amount of particulate/detritus ingestion was included based on the benthic feeding habits of white perch, but the ingestion of sediment solids is assumed to be negligible.</p> <p><b>Benthic invertebrates</b> – Perch are assumed to consume primarily amphipods (DETs), shrimp (both C/Os and DETs), and some annelids (DETs and DEPs).</p> <p><b>Small fish</b> – Perch are assumed to consume mostly benthic small forage fish because they are primarily benthic feeders but may also consume some filter-feeding fish.</p>
Particulates/detritus (near-bottom)	uniform	5	0 – 10	5	
Phytoplankton/algae	uniform	2	0 – 20	2	
Zooplankton	uniform	3	0 – 20	3	
Benthic invertebrates	uniform	75	0 – 100	75	
DEPs <sup>f</sup>	uniform	10	0 – 20	10	
DETs <sup>f</sup>	uniform	60	50 – 100	60	
C/Os <sup>f</sup>	uniform	30	0 – 50	30	
Small fish	uniform	15	0 – 90	15	
Filter feeding fish <sup>j</sup>	uniform	25	0 – 50	25	
Small forage fish <sup>j</sup>	uniform	75	50 – 100	75	

**Table 11. Parameter distributions and rationale for the selection of species-specific diets**

Prey Items by Model Compartment	Distribution Type	Nominal Value (%)	Range (%)	Calibrated Value (%)	Rationale and Source <sup>b</sup>
<b>American Eel</b>					
Sediment solids	uniform	2	0 – 5	2	<b>General</b> – The diet of the American eel is diverse, consisting of crabs, crayfish, bivalves, polychaetes, insects, gastropods, and fish (Ogden 1970; Lookabaugh and Angermeier 1992; Wenner and Musick 1975; Denoncourt and Stauffer 1993). (Ogden 1970; Lookabaugh and Angermeier 1992; Wenner and Musick 1975)(Ogden 1970; Lookabaugh and Angermeier 1992; Wenner and Musick 1975)(Ogden 1970; Lookabaugh and Angermeier 1992; Wenner and Musick 1975) As American eel grow larger, fish and crustaceans (i.e., crayfish or crab) become more important components of their diet than do aquatic insects and other benthic invertebrates (Lookabaugh and Angermeier 1992; Ogden 1970). Selected prey portions are based on larger fish representing higher-trophic-level feeders; prey portions for American eel > 50 cm were evaluated (see Attachment 4 for additional details).
Particulates/detritus (near-bottom)	uniform	3	0 – 5	3	
Benthic invertebrates	uniform	55	0 – 60	55	
DEPs <sup>f</sup>	uniform	10	0 – 40	10	
DETs <sup>f</sup>	uniform	20	0 – 40	20	<b>Sediment</b> – Data on sediment consumption were not available, but a small amount of sediment and particulate/detritus ingestion was included based on the benthic feeding habits of eel.
C/Os <sup>f</sup>	uniform	70	30 – 100	70	
Small fish	uniform	40	20 – 60	40	<b>Benthic invertebrates</b> – Ogden (1970) reported that the size of invertebrates found in eel stomachs increased with increasing eel size. Within each size class, organisms were generally present in proportions related to those found in bottom sediment. Eel were assumed to consume predominantly crayfish (C/Os), followed by gastropods and bivalves (DETs) and polychaetes/oligochaetes (DEPs). Although biomass data indicate a high portion of DETs in the LPRSA relative to C/Os, the biomass evaluation did not account for a number of mobile C/Os, such as small blue crabs or rock crabs, which represent their preferred prey.
Filter-feeding fish <sup>l</sup>	uniform	25	0 – 50	25	
Small forage fish <sup>l</sup>	uniform	75	50 – 100	75	<b>Small fish</b> – American eels are primarily bottom feeders, and thus the fish portion of their diet is composed mostly of benthic small forage fish (Ogden 1970).

**Table 11. Parameter distributions and rationale for the selection of species-specific diets**

Prey Items by Model Compartment	Distribution Type	Nominal Value (%)	Range (%)	Calibrated Value (%)	Rationale and Source <sup>b</sup>
<b>Bass (Smallmouth/Largemouth)</b>					
Sediment solids	point est.	0	na	0	<b>General</b> – Both smallmouth and largemouth bass are considered to be opportunistic predators that will generally consume prey relative to their abundance in the environment. Smallmouth bass consume primarily fish and crayfish; other smaller components of their diet may include insects, other crustaceans, mollusks, and worms (George and Hadley 1979; Turner 1966a; Wydoski and Whitney 1979). Adult largemouth bass are predominately piscivorous and eat a variety of small fish (e.g., bluegills, minnows, perch, and shiners) but are also opportunistic and eat crayfish, frogs, insects, snakes, and even small mammals and birds that enter the water (Scott and Crossman 1973). A Hudson River study found that 75 to 90% of the largemouth bass diet consisted of fish, and 10 to 25% consisted of various invertebrates, including crayfish (TAMS and Menzie-Cura 2000). The invertebrates most commonly observed in the gut contents of largemouth bass included amphipods, isopods, cladocerans, copepods, ostracods, and some annelid larvae (TAMS and Menzie-Cura 2000).
Particulates/detritus (near-bottom)	point est.	0	na	0	
Benthic invertebrates	uniform	80	0 – 100	80	
DEPs <sup>e</sup>	point est.	0	na	0	
DETs <sup>e</sup>	uniform	20	0 – 100	20	<b>Sediment</b> – Bass spend most of their time in the pelagic zone, and thus their ingestion of sediment solids or particulates/detritus is assumed to be negligible.
C/Os <sup>e</sup>	uniform	80	60 – 100	80	
Small fish	uniform	80	20 – 100	80	<b>Benthic invertebrates</b> – Bass are assumed to consume primarily crayfish (C/Os) and a small portion of mollusks (DETs) based on their feeding habits and information regarding their preferred invertebrate prey types (Attachment 4).
Filter-feeding fish <sup>i</sup>	uniform	50	0 – 100	50	
Small forage fish <sup>j</sup>	uniform	50	0 – 100	50	<b>Small fish</b> – Bass were assumed to consume small forage fish and filter-feeding fish in equal proportions, although the actual dietary portions are likely based on the availability and abundance of these types of small fish in the LPRSA.

<sup>a</sup> For triangular distributions, the nominal value is the most likely value, and the range defines the maximum and minimum values.

<sup>b</sup> Additional details on the rationale and sources for the fish dietary assumptions are provided in Attachment 4.

<sup>c</sup> Examples of small benthic invertebrate DEPs include *Limnodrilus hoffmeisteri* and various polychaete/polychaete worms. Deposit feeders that selectively consume rich detrital material at the sediment surface are classified as DETs.

<sup>d</sup> Examples of small benthic invertebrate DETs include bivalves (e.g., clams), gastropods, polychaetes, amphipods, and some insects.

<sup>e</sup> Examples of benthic invertebrate C/Os include turbellaria, nematode, leeches, larger insects, decapods (e.g., crayfish and shrimp), and some large polychaetes.

<sup>f</sup> The dietary percentages for DETs, DEPs, and C/Os represent the percentage of each within the invertebrate dietary compartment.

<sup>g</sup> Examples of filter-feeding fish include young-of-the-year Atlantic menhaden and small gizzard shad.

<sup>h</sup> Examples of small forage fish include mummichog, shiners, striped mullet, and tessellated darter.

<sup>i</sup> Invertebrate consumption rates for this species are based on relative biomass in the LPRSA for the relevant modeling year.

<sup>j</sup> The dietary percentages for small forage fish and filter-feeding fish represent the percentage of each within the small fish dietary compartment.

C/O – carnivore/omnivore

DNR – Department of Natural Resources

UFGS – United Geological Survey

DEP – deposit feeder

LPRSA – Lower Passaic River Study Area

DET – detritivore

RM – river mile

## 8 SOURCES OR DATA ANALYSIS BEHIND ORGANISM WEIGHT AND LIPID CONTENT ASSUMPTIONS

USEPA requested information on the sources or data analysis behind organism weight and lipid content assumptions used in the bioaccumulation model. Sources for the weight and lipid fraction of each model compartment are included in Table 12.

**Table 12. Species-specific non-dietary fraction parameter distributions and rationale**

Parameter by Model Compartment	Unit	Modeling Area	Nominal Value	Distribution Type	Distribution Value <sup>a</sup>	Calibrated Value	Source Notes
<b>Phytoplankton/Algae</b>							
Lipid fraction of organism	fraction	site-wide	0.0012	triangle	0.0008 – 0.002	0.0012	Mackintosh et al. (2004)
<b>Zooplankton</b>							
Weight	kg	site-wide	$1.4 \times 10^{-7}$	point	na	$1.4 \times 10^{-7}$	Giles and Cordell (1998); could range from $3.3 \times 10^{-8}$ to $2.3 \times 10^{-7}$
Lipid fraction of organism	fraction	site-wide	0.01	triangle	0.009 – 0.011	0.01	Evjemo and Olsen (1997)
<b>Benthic Invertebrate DEPs<sup>b</sup></b>							
Weight	kg	site-wide	$2.0 \times 10^{-6}$	triangle	$2.4 \times 10^{-7}$ to $5.8 \times 10^{-6}$	$2.0 \times 10^{-6}$	Weighted average of literature-based value for species within the DEP model compartment; range based on minimum to maximum values for component species representing 1% or more of the total DEP biomass (no range was available for lipid fraction and water content, and thus point estimates were used)
Lipid fraction of organism	fraction	site-wide	0.020	triangle	na	0.020	
<b>Benthic Invertebrate DETs<sup>c</sup></b>							
Weight	kg	site-wide	$1.2 \times 10^{-4}$	triangle	$3.3 \times 10^{-5}$ to $3.3 \times 10^{-4}$	$1.2 \times 10^{-4}$	Weighted average of literature-based value for species within the DET model compartment; range based on minimum to maximum values for component species representing 1% or more of the total DET biomass
Lipid fraction of organism	fraction	site-wide	0.015	triangle	0.009 – 0.026	0.015	
<b>Benthic Invertebrate C/Os<sup>d</sup></b>							
Weight	kg	site-wide	$1.6 \times 10^{-5}$	triangle	$2.5 \times 10^{-6}$ to $7.2 \times 10^{-5}$	$1.6 \times 10^{-5}$	Weighted average of literature-based value for species within C/O model compartment. Range based on minimum to maximum values for component species representing 1% or more of the total C/O biomass
Lipid fraction of organism	fraction	site-wide	0.023	triangle	0.013 – 0.061	0.023	
<b>Filter-Feeding Fish<sup>e</sup></b>							
Weight	kg	site-wide	0.057	normal	SD = 0.020	0.057	Based on LPRSA gizzard shad data (n = 115); range of 0.009 to 0.106 kg (lengths ranged from 67 to 111 mm), which reflects the size of fish expected to be consumed by higher-trophic level species; juvenile (young-of-the-year)
Lipid fraction of organism	fraction	site-wide	0.022	normal	SD = 0.0217	0.022	LPRSA gizzard shad data (n = 3); range of 0.019 to 0.026

**Table 12. Species-specific non-dietary fraction parameter distributions and rationale**

Parameter by Model Compartment	Unit	Modeling Area	Nominal Value	Distribution Type	Distribution Value <sup>a</sup>	Calibrated Value	Source Notes
<b>Small Forage Fish<sup>1</sup></b>							
Weight	kg	site-wide	0.0031	normal	SD = 0.000069	0.0031	LPRSA mummichog data (n = 1,416); range of 0.0005 to 0.016 kg (lengths ranged from 28 to 100 mm), which reflects the size of fish expected to be consumed by higher-trophic-level species
Lipid fraction of organism	fraction	site-wide	0.022	normal	SD = 0.0015	0.022	LPRSA small forage fish tissue data (n = 25); range of 0.014 to 0.043
<b>Blue Crab</b>							
Weight	kg	site-wide	0.16	normal	SD = 0.0039	0.16	LPRSA tissue data (n = 214); range of 0.024 to 0.35 kg (lengths ranged from 114 to 179 mm)
Lipid fraction of organism	fraction	site-wide	0.012	normal	SD = 0.00064	0.012	LPRSA tissue data (n = 24); range of 0.0072 to 0.020
<b>Carp</b>							
Weight	kg	RM 4-17.4	3.1	normal	SD = 0.14	3.1	LPRSA tissue data (n = 12); range of 2.2 to 3.9 kg (lengths ranged from 524 to 610 mm)
Lipid fraction of organism	fraction	RM 4-17.4	0.054	normal	SD = 0.0046	0.054	LPRSA tissue data (n = 12); range of 0.028 to 0.081
<b>Catfish</b>							
Weight	kg	RM 4-17.4	0.88	normal	SD = 0.062	0.88	LPRSA tissue data (n = 30) for white and channel catfish; range of 0.422 to 1.695 kg (lengths ranged from 315 to 541 mm)
Lipid fraction of organism	fraction	RM 4-17.4	0.058	normal	SD = 0.0043	0.058	LPRSA tissue data (n = 30) for white and channel catfish; range of 0.017 to 0.11
<b>White Perch</b>							
Weight	kg	site-wide	0.081	normal	SD = 0.0091	0.081	LPRSA tissue data (n = 65); range of 0.028 to 0.54 kg (lengths ranged from 118 to 321 mm)
Lipid fraction of organism	fraction	site-wide	0.045	normal	SD = 0.0039	0.045	LPRSA tissue data (n = 20); range of 0.013 to 0.090
<b>American Eel</b>							
Weight	kg	site-wide	0.14	normal	SD = 0.022	0.14	LPRSA tissue data (n = 43); range of 0.028 to 0.452 kg (lengths ranged from 264 to 635 mm)
Lipid fraction of organism	fraction	site-wide	0.065	normal	SD = 0.0056	0.065	LPRSA tissue data (n = 21); range of 0.025 to 0.12

**Table 12. Species-specific non-dietary fraction parameter distributions and rationale**

Parameter by Model Compartment	Units	Modeling Area	Nominal Value	Distribution Type	Distribution Value <sup>a</sup>	Calibrated Value	Source Notes
<b>Bass</b>							
Weight	kg	RM 6-17.4	0.25	normal	SD = 0.13	0.25	LPRSA tissue data (n = 11) for smallmouth and largemouth bass; range of 0.109 to 0.440 kg (lengths ranged from 190 to 319 mm)
Lipid fraction of organism	fraction	RM 6-17.4	0.024	normal	SD = 0.0029	0.024	LPRSA tissue data (n = 6) for smallmouth and largemouth bass; range of 0.021 to 0.029

<sup>a</sup> For triangular distributions, the nominal value is the most likely value, and the range defines the maximum and minimum values. For normal distributions, the mean of the distribution (and the raw data) is provided as the nominal value column, and the SE of the raw data defines the SD of the uncertainty distribution of the sample average. Consistent with the Central Limit Theorem, estimates of the mean are expected to approximate a normal distribution, with the mean of the distribution defined by the mean of the raw data and the SD of the distribution defined as the SE of the raw data.

<sup>b</sup> DEPs are represented by the oligochaete *Lumbricus variegatus*.

<sup>c</sup> DETs include aquatic insects such as chironomids, amphipods, and bivalves that feed on detritus, either suspended or newly settled.

<sup>d</sup> C/Os are represented by *Neris virens*.

<sup>e</sup> Examples of filter-feeding fish include young-of-the-year Atlantic salmon and small gizzard shad.

<sup>f</sup> Examples of small forage fish include mummichog, shiners, and tessellated darter.

AE – absorption efficiency

BPJ – best professional judgment

C/O – benthic invertebrate carnivore/omnivore

DEP – benthic invertebrate deposit feeder

DET – benthic invertebrate detritivore

LPRSA – Lower Passaic River Study Area

na – not applicable

NLOC – non-lipid organic carbon

NLOM – non-lipid organic matter

RM – river mile

SD – standard deviation

SE – standard error

tetraCB – tetrachlorobiphenyl

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# ATTACHMENT 1. SUPPORTING DATA FOR FISH AND CRAB PARAMETERIZATION

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Preliminary

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Preliminary

## 1 Introduction

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This attachment summarizes the Lower Passaic River Study Area (LPRSA) analytical data available for blue crab and the selected fish species modeled in the LPRSA bioaccumulation model. Also included is additional detail regarding the justification for the selection of empirical data used to calibrate the bioaccumulation model.

## 2 Overview of LPRSA Fish Sample Compositing and Analysis

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LPRSA fish tissue samples were collected during 2009 and 2010 sampling events (Windward 2010a, [in prep]-c).

In August and September 2009, a large number of blue crab and fish representing numerous fish species were collected from the LPRSA (Windward 2010a). The compositing plan for crab and fish collected in 2009 was agreed upon by the Cooperating Parties Group (CPG) and the US Environmental Protection Agency (USEPA) during multiple meetings from January through June of 2010, as documented in multiple memoranda and tables as follows:

- The *Revised Sample Analysis Plan for Blue Crab Tissue for the Lower Passaic River Restoration Project* memorandum (Windward 2010b) (approved by USEPA on February 8, 2010)
- The *Revised Sample Analysis Plan for Catfish, Bullhead, Carp, Bass, White Sucker, and Northern Pike Tissue for the Lower Passaic River Restoration Project (Revised Fish Sample Analysis Plan, Part 1)* memorandum (Windward 2010e) (approved by USEPA on May 21, 2010)
- The final white perch and American eel analytical plan tables (Windward 2010c, d) (approved by USEPA on June 15, 2010)

In response to USEPA's comments (Vaughn 2010) on the CPG's November 6, 2009, proposed fish analysis plan (Windward 2009a), fish collected in 2009 were analyzed as individuals, rather than composites, when possible (i.e., when the fish collected were large enough for analysis as individual fish). Individual fish analyzed as whole-body samples had to weigh a minimum of approximately 150 g to meet analytical mass requirements, and individual fish analyzed as fillet samples had to weigh a minimum of approximately 450 g<sup>1</sup> to meet analytical mass requirements. Consequently, a mix of individual and composite fish samples were analyzed, depending on the size of fish collected. In addition, the whole-body fish dataset included samples analyzed as

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<sup>1</sup> An individual fish weight greater than 450 g was selected based on the assumption that fish fillet mass makes up one-third (33.3%) of whole-body fish mass. A whole-body sample mass of 450 g is therefore needed to achieve an estimated fillet mass that meets minimum mass requirements (i.e., 150 g).

whole-body samples, as well as samples that were mathematically reconstituted using fillet and carcass weights and concentrations<sup>2</sup> (i.e., reconstituted whole-body samples). For blue crab, whole-body samples were mathematically reconstituted using muscle/hepatopancreas and carcass weights and concentrations (i.e., reconstituted whole-body samples).

Between June and August 2010, small forage fish were collected from the LPRSA. Small forage fish specimens were composited according to a USEPA-approved compositing memorandum:

- The *Revised Analysis Plan for the Small Forage Fish Tissue Samples* (Windward 2010) (approved by USEPA during the teleconference calls on August 5, 2010, and finalized per USEPA comments received October 25 and 26, 2010)

Table 2-1 summarizes the fish and blue crab samples analyzed from the LPRSA based on 2009 and 2010 sampling.

**Table 2-1. Summary of LPRSA fish and blue crab samples**

Fish Species	Sample Type	Tissue Type			
		Fillet	Carcass	Whole Body (reconstituted)	Whole Body
Gizzard shad <sup>a</sup>	composite		0	0	3
Mummichog	composite		0	0	18
Other small forage fish <sup>b</sup>	composite		0	0	9
Blue crab	composite	0	24	24 <sup>c</sup>	0
Carp	individual	12	0	0	12
Brown bullhead <sup>a</sup>	individual	0	6	0	6
Channel catfish	individual		11	11	0
White catfish	individual	19	19	19	0
White sucker <sup>a</sup>	individual	5	5	5	0
White perch	individual	2	1	1	4
	composite	17	-		15
	<b>Total</b>	<b>19</b>	<b>1</b>	<b>1</b>	<b>19</b>
American eel	individual	17	1		12
	composite	15	1	1	7
	<b>Total</b>	<b>32</b>	<b>2</b>		
Largemouth bass	individual	2	2	2	0
	composite	1	1	1	0
	<b>Total</b>	<b>3</b>	<b>3</b>	<b>3</b>	
Smallmouth bass	composite	3	3	3	
Northern pike <sup>a</sup>	individual	1	1	1	

<sup>2</sup> All tissue chemical concentrations are reported on a wet weight basis.

- <sup>a</sup> These species were not modeled explicitly in the bioaccumulation model, but these data were considered as part of the uncertainty assessment.
- <sup>b</sup> Includes the following small forage fish samples: white perch (n = 2 samples), pumpkinseed (n = 1), silver shiner (n = 1), spottail shiner (n = 1), and mixed forage fish (n = 4). Gizzard shad were also analyzed but were not included as small forage fish samples in the bioaccumulation model, since gizzard shad are more representative of filter-feeding fish, which were modeled as a separate compartment in the bioaccumulation model.
- Reconstructed whole-body tissue concentrations for blue crab were calculated using muscle/hepatopancreas and corresponding carcass concentrations.
- LPRSA – Lower Passaic River Study Area

### 3 Fish and Crab Data Used to Calibrate the Bioaccumulation Model

This section describes the data used to calibrate the bioaccumulation model for blue crab and each of the selected fish compartments. Tables 3-1 and 3-2 summarize the available whole-body data that were used to calibrate the bioaccumulation model. Figures in the following subsections are presented for 2,3,7,8-tetrachlorodibenzo-*p*-dioxin (TCDD) and total polychlorinated biphenyl (PCB) congeners. Tetrachlorobiphenyl concentration patterns were found to be similar to that of total PCB congeners.

**Table 3-1. Summary of analytical tissue samples used for model calibration**

LPRSA Area	Number of Whole-Body Samples											
	Blue crab		Common Carp		White Perch		Catfish <sup>a</sup>		American Eel		Bass <sup>b</sup>	
	C	I	C	I	C	I	C	I	C	I	C	I
RM 0 – RM 2 (Reach 1)	8	-	-	-	-	2	-	-	1	1	-	-
RM 2 – RM 4 (Reach 2)	6	-	-	-	1	-	0 <sup>c</sup>	-	1	-	-	-
RM 4 – RM 6 (Reach 3)	4	-	-	0 <sup>d</sup>	6	-	4	-	3	-	-	-
RM 6 – RM 8 (Reach 4)	4	-	-	2	2	-	1	-	4	1	-	-
RM 8 – RM 10 (Reach 5)	2	-	-	2	3	-	3	1	2	2	1	-
RM 10 – RM 12 (Reach 6)	-	-	-	2	-	1	-	7	-	2	-	-
RM 12 – RM 14 (Reach 7)	-	-	-	2	1	1	-	-	1	-	-	-
RM 14 – RM 17.4 (Reach 8)	-	-	-	2	3	-	10	-	-	1	1	-
Site-wide total	24	0	0	10	15	5	0	20	13	4	2	-
	24		10		20		29		21			

<sup>a</sup> Includes white catfish and channel catfish.

<sup>b</sup> Includes smallmouth and largemouth bass.

<sup>c</sup> One individual catfish sample was collected between RM 2 and RM 4; however, this sample was excluded from the calibration dataset because it was collected outside of the modeling area identified for catfish.

<sup>d</sup> Two individual carp samples were collected between RM 4 and RM 6; however, these samples were excluded from the calibration dataset because they were collected outside of the modeling area identified for carp.

C – composite fish sample  
I – individual fish sample

LPRSA – Lower Passaic River Study Area  
RM – river mile

**Table 3-2. Summary of empirical fish and crab tissue concentrations for model calibration**

Species	Modeling Area	No. of Samples	Concentration <sup>a</sup>					
			2,3,7,8-TCDD (ng/kg ww)		Tetrachlorobiphenyl (µg/kg ww)		Total PCB Congeners (µg/kg ww)	
			Mean	SD	Mean	SD	Mean	SD
Blue crab	site-wide <sup>b</sup>	24	51	16	59	14	320	100
Carp	RM 7 - RM 17.4	10 <sup>c</sup>	430	420	1,100	620	4,300	2,200
Catfish <sup>d</sup>	RM 4 - RM 17.4	29 <sup>e</sup>	130	100	370	250	2,200	1,600
White perch	site-wide	20	130	70	470	250	2,100	1,200
American eel	site-wide	21	18 <sup>f</sup>	14 <sup>f</sup>	180	110	1,500	1,200
Bass <sup>g</sup>	RM 17.4	6	60	66	280	190	2,400	2,800

<sup>a</sup> Concentrations are based only on detected concentrations (i.e., all samples in the dataset had detected concentrations), except for American eel and 2,3,7,8-TCDD.

<sup>b</sup> Whole-body concentrations in blue crab collected from RM 0 to RM 10 were used to represent site-wide concentration.

<sup>c</sup> Two carp samples collected between RM 4 and RM 6 were excluded from the calibration dataset because they were collected outside of the modeling area identified for carp. The effect of excluding these samples was addressed in the uncertainty analysis.

<sup>d</sup> Includes white catfish and channel catfish.

<sup>e</sup> One catfish sample collected between RM 2 and RM 4 was excluded from the calibration dataset because it was collected outside of the modeling area identified for catfish. The effect of excluding this sample was addressed in the uncertainty analysis.

<sup>f</sup> Summary statistics include one non-detected value in Reach 8 (RM 14 to RM 17.4).

<sup>g</sup> Includes smallmouth and largemouth bass.

PCB – polychlorinated biphenyl

RM – river mile

SD – standard deviation

TCDD – tetrachlorodibenzo-*p*-dioxin

ww – wet weight

### 3.1 BLUE CRAB

Adult blue crab (*Callinectes sapidus*) were included in the bioaccumulation model separately from the small benthic invertebrate compartments. Blue crab whole-body concentrations were estimated based on mathematically reconstituted muscle-hepatopancreas and carcass samples based on crab collected from Reach 1 through 5 (river mile [RM] 0 to RM 10). Per the fish / decapod quality assurance project plan (QAPP) (Windward 2009b) and blue crab compositing plan (Windward 2010), carcass samples were analyzed above RM 10, although 17 muscle/hepatopancreas crab samples were analyzed above RM 10. The blue crab muscle/hepatopancreas samples collected above RM 10 were of similar size as those collected below RM 10 (Figures 3-1 and 3-2).<sup>3</sup>

<sup>3</sup> Only reconstituted whole-body data were used in the bioaccumulation model calibration. However, for informational purposes, Figures 3-1 and 3-2 also show crab sizes for muscle-hepatopancreas data, and Figures 3-3 and 3-4 show concentrations for muscle-hepatopancreas data.

Figures 3-3 through 3-8 present concentrations of 2,3,7,8-TCDD and total PCBs in blue crab whole-body samples. The whole-body data based on blue crab collected from RM 0 to RM 10 were assumed to be representative of site-wide concentrations (i.e., concentrations in crab from RM 0 to RM 17.4) for the purposes of calibrating the bioaccumulation model. However, muscle-hepatopancreas concentrations (which were available from throughout the LPRSA) were slightly less in Reaches 6 through 8 (i.e., above RM 10) than in Reaches 1 through 5 (i.e., below RM 10). In addition, average concentrations of muscle-hepatopancreas based on data from the entire LPRSA were less than those based on data from Reach 1 through 5 (Table 3-3). Therefore, the site-wide whole-body concentrations used as the basis for calibration for blue crab (i.e., samples collected from Reaches 1 to 5 [below RM 10]) may slightly overestimate concentrations in blue crab collected in the upper freshwater portion of the LPRSA (i.e., between Reaches 6 and 8 [above RM 10]).

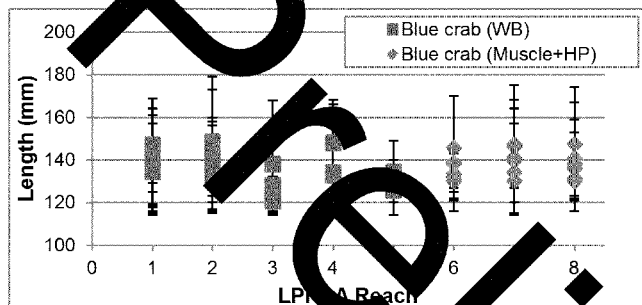
**Table 3-3. Comparison of LPRSA blue crab combined muscle-hepatopancreas concentrations**

LPRSA	Combined Muscle-Hepatopancreas Concentration				
		Total PCBs (µg/kg ww)		2,3,7,8-TCDD (ng/kg ww)	
	Concentration	Range	Average	Range	Average
RM 0 to RM 10 (Reaches 1 to 5)	4	10 – 790	371	24 – 110	61
RM 10 to RM 17.4 (Reaches 6 to 8)	17	4 – 110	261	4 – 71	33
RM 0 to RM 17.4 (Reaches 1 to 8)	41	76 – 79	326	4 – 110	49

<sup>a</sup> Reconstituted whole-body data based on muscle-hepatopancreas and carcass samples from this LPRSA area (RM 0 to RM 10) were used to calibrate the model for site-wide concentrations. No carcass data were analyzed based on crab collected above RM 10.

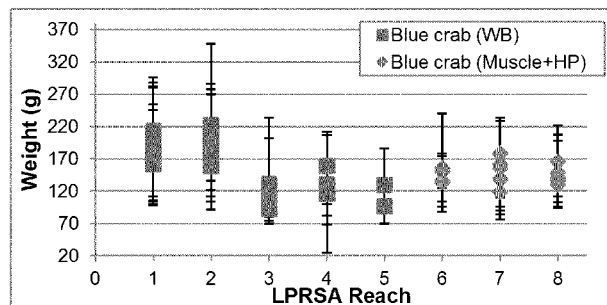
LPRSA – Lower Passaic River Study Area  
 PCB – polychlorinated biphenyl  
 RM – river mile

TCDD – tetrachloro-dibenzo-*p*-dioxin  
 ww – wet weight



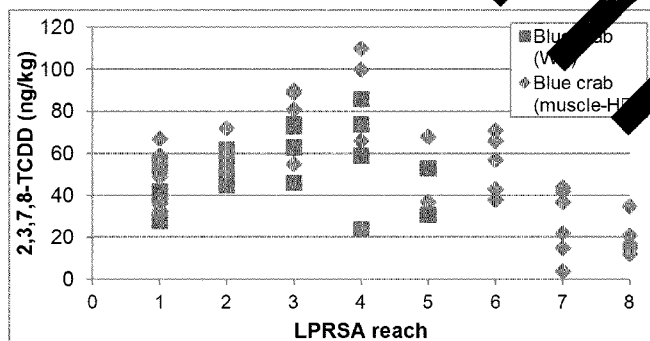
Note: Bars represent minimum and maximum values in composite sample. Muscle+hepatopancreas (HP) data above Reach 5 are shown for informational purposes; only whole-body data were used to calibrate the bioaccumulation model.

**Figure 3-1. Mean length of blue crab in analytical composite samples**



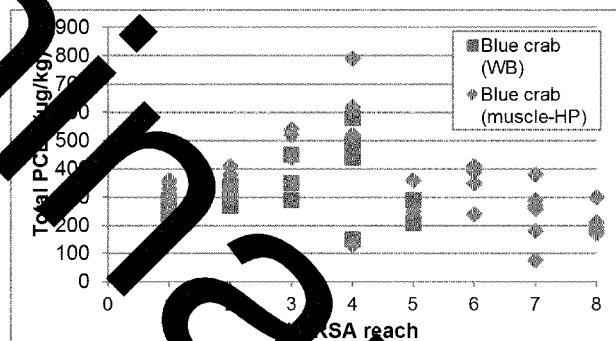
Note: Bars represent minimum and maximum values in composite sample. Muscle+hepatopancreas (HP) data above Reach 5 are shown for informational purposes; only whole-body data were used to calibrate the bioaccumulation model.

**Figure 3-2. Mean weight of blue crab in analytical composite samples**



Note: Muscle/hepatopancreas (HP) data above Reach 5 are shown for informational purposes; only whole-body data were used to calibrate the bioaccumulation model.

**Figure 3-3. Blue crab whole-body 2,3,7,8-TCDD concentrations by LPRSA reach**



Note: Muscle/hepatopancreas (HP) data above Reach 5 are shown for informational purposes; only whole-body data were used to calibrate the bioaccumulation model.

**Figure 3-4. Blue crab whole-body total PCB concentrations by LPRSA reach**

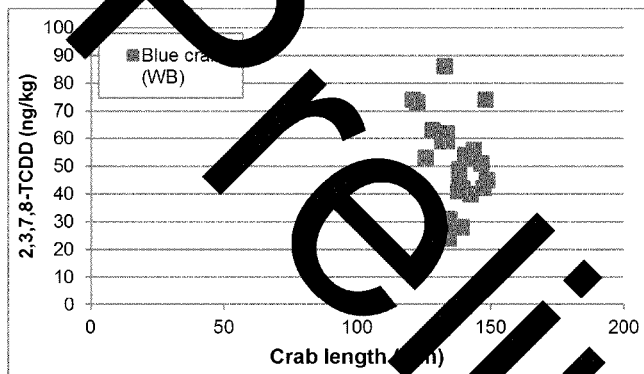


Figure 3-5. Blue crab length and whole-body 2,3,7,8-TCDD concentrations

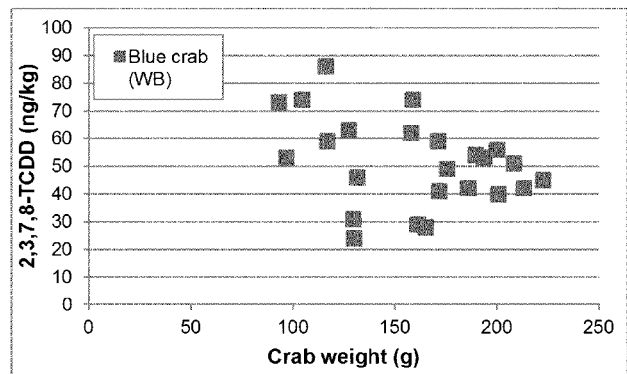


Figure 3-6. Blue crab weight and whole-body 2,3,7,8-TCDD concentrations

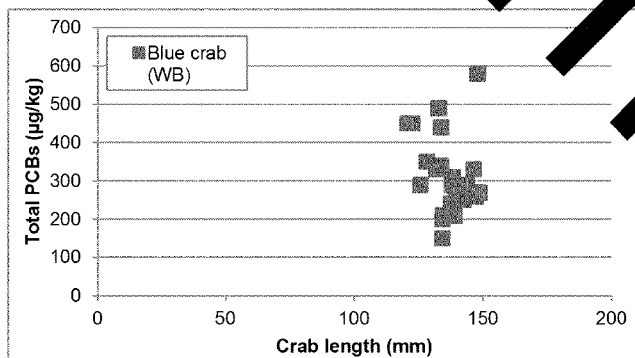


Figure 3-7. Blue crab length and whole-body total PCB concentrations

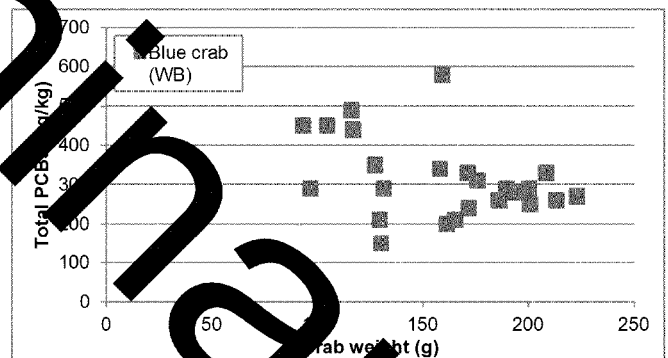


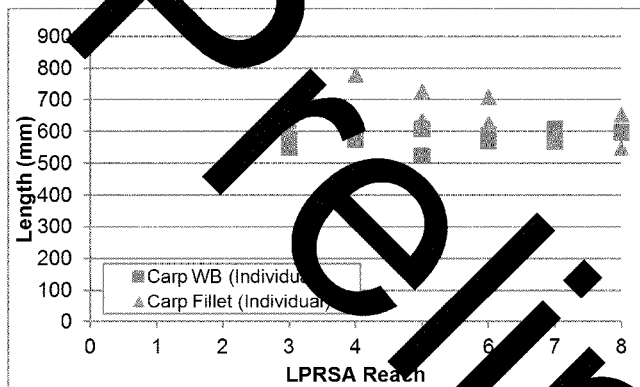
Figure 3-8. Blue crab weight and whole-body total PCB concentrations

### 3.2 CARP

Carp (*Cyprinus carpio*) are modeled in a compartment separate from benthic omnivores/ invertivores (catfish) in the bioaccumulation model because carp represent a unique exposure pathway based on their size, age, and feeding ecology.

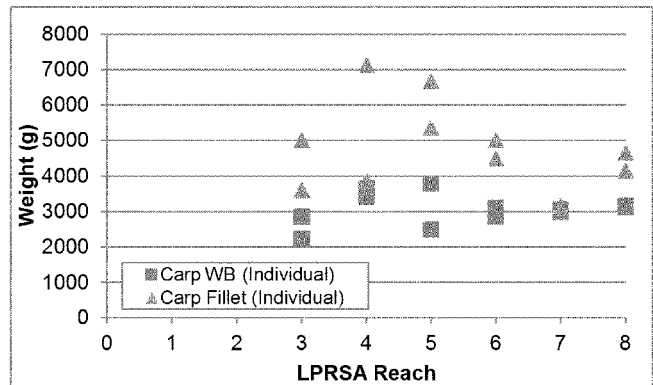
Carp tissue data were analyzed as individual fish collected from LPRSA Reaches 3 through 8 (RM 4 to RM 17.4). Both carp fillet and whole-body samples were collected (from different fish) and analyzed.<sup>4</sup> Carp analyzed as fillets were generally larger (in length and weight) than those analyzed as whole-body samples (Figures 3-9 and 3-10). Only carp whole-body data were used in the bioaccumulation model calibration, although Figures 3-9 and 3-10 show fish sizes for fillet data for informational purposes. Figures 3-4 through 3-16 present carp whole-body 2,3,7,8-TCDD and total PCB concentrations. Note that only samples from Reaches 4 to 8 (RM 6 to RM 17.4) were included in the calibration dataset, consistent with the modeling area for carp. Thus, the two samples collected downstream of RM 6 were not included in the calibration data. However, data from these samples are presented in Figures 3-9 through 3-16 for informational purposes.

<sup>4</sup> For some other LPRSA fish for which fillets were analyzed, the fillet and carcass data were derived from the same fish, and these data were mathematically reconstituted to derive whole-body concentration data.



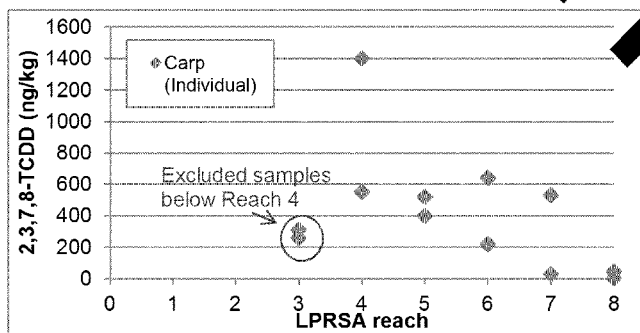
Note: Fillet data and whole-body (WB) data below Reach 4 are shown for informational purposes; only whole-body data from Reach 4 and above were used to calibrate the bioaccumulation model.

**Figure 3-9. Length of individual carp in analytical samples by LPRSA reach**

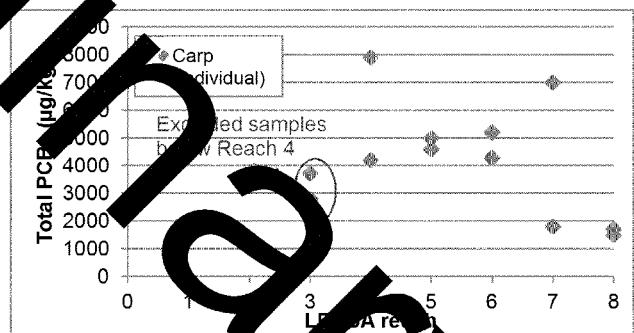


Note: Fillet data and whole-body (WB) data below Reach 4 are shown for informational purposes; only whole-body data from Reach 4 and above were used to calibrate the bioaccumulation model.

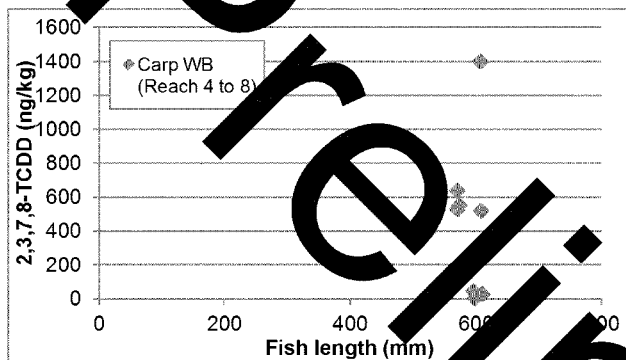
**Figure 3-10. Weight of individual carp in analytical samples by LPRSA reach**



**Figure 3-11. Carp whole-body 2,3,7,8-TCDD concentrations by LPRSA reach**

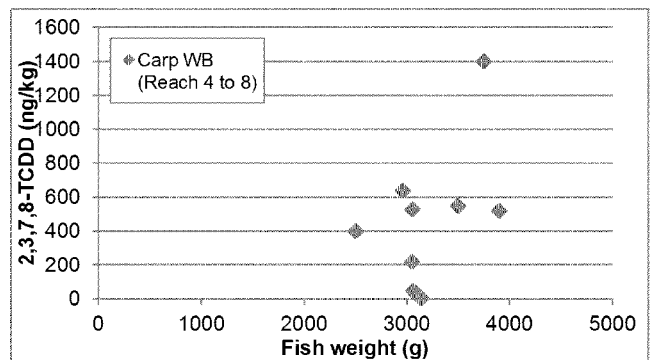


**Figure 3-12. Carp whole-body total PCB concentrations by LPRSA reach**



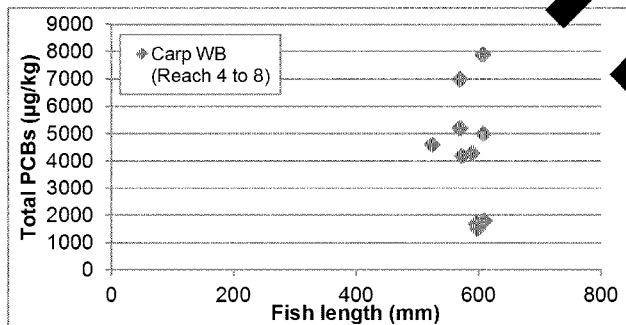
Note: Graph presents only carp data included in calibration dataset.

**Figure 3-13. Carp length and whole-body 2,3,7,8-TCDD concentrations**



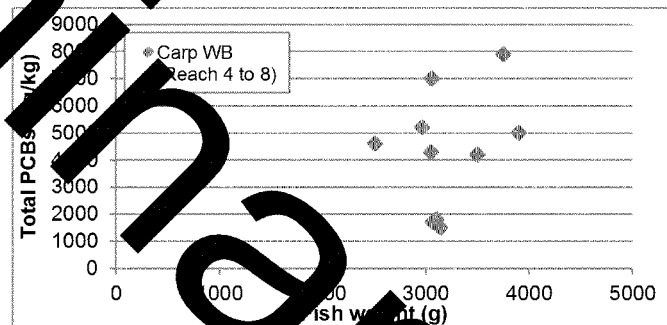
Note: Graph presents only carp data included in calibration dataset.

**Figure 3-14. Carp weight and whole-body 2,3,7,8-TCDD concentrations**



Note: Graph presents only carp data included in calibration dataset.

**Figure 3-15. Carp length and whole-body total PCB concentrations**



Note: Graph presents only carp data included in calibration dataset.

**Figure 3-16. Carp weight and whole-body total PCB concentrations**

### 3.3 CATFISH

The catfish compartment of the bioaccumulation model included both white catfish (*Ictalurus catus*) and channel catfish (*Ictalurus punctatus*). These catfish species have similar life histories and diets. In addition, the channel and white catfish collected in the LPRSA were similar in size (see Figures 3-17 and 3-18). Both channel and white catfish are opportunistic feeders that prey on whatever is available, including larger invertebrates such as amphipods, crayfish, and mollusks, as well as insects and small fish (NODEP 2001; Wellborn 1988; California Fish Website 2013; Turner 1966b). Both white and channel catfish are predominately benthic feeders that consume some portion of sediment and detritus in their diet. Channel catfish have a lower tolerance for salinity than do white catfish, and therefore may have a smaller exposure area within the LPRSA than do white catfish.<sup>5</sup> White catfish were collected in the lower portions of the LPRSA (below RM 8<sup>6</sup>), where there is higher salinity.

Only white and channel catfish whole-body (i.e., reconstituted) data were evaluated in the bioaccumulation model calibration. Catfish whole-body data were based on the analysis of individual fish for bone, fillet and carcass tissue. Whole-body concentrations were mathematically reconstituted based on the fillet and carcass weights and chemical concentrations.

Figures 3-19 through 3-24 present catfish whole-body tissue 2,3,7,8-TCDD and total PCB concentrations. Although concentrations for white catfish collected in Reaches 2 through 4 ranged greater than those for white and channel catfish collected in Reaches 5 through 8, average concentrations in white and channel catfish were similar in areas of the LPRSA where both species were collected. Only samples from Reaches 3 to 8 (i.e., RM 4 to RM 17.4) were included in the calibration dataset, consistent with the modeling area for catfish. Thus, the one sample collected downstream of RM 4 was not included in the calibration dataset; however, data from this sample are presented in Figures 3-17 through 3-24 for informational purposes.

<sup>5</sup> Whitecatfish were reported to be the dominant species in Chesapeake Bay tributaries with salinities up to 12 ppt (Kendall and Schwartz 1968), which demonstrates a moderate salinity tolerance. Channel catfish have a lower salinity tolerance and prefer salinities less than 4 ppt (FAO 2014). Although they can tolerate moderate salinities (up to 11 ppt) (FAO 2014; McMahon and Terrell 1982; Avault et al. 1969).

<sup>6</sup> LPRSA Reach 5 extends from RM 8 to RM 10.

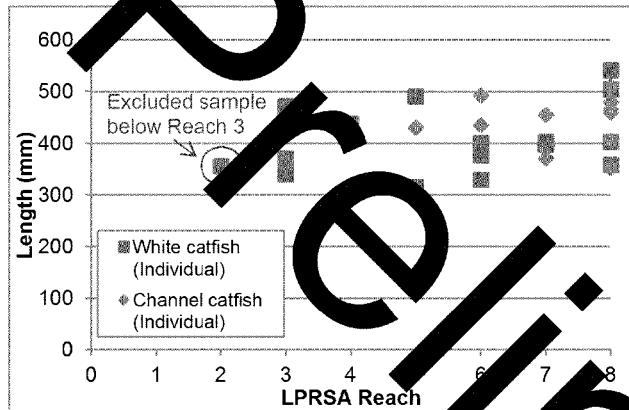


Figure 3-17. Length of individual catfish in analytical samples by LPRSA reach

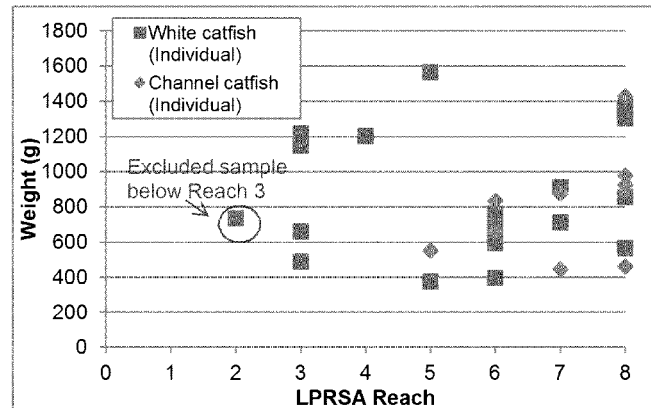


Figure 3-18. Weight of individual catfish in analytical samples by LPRSA reach

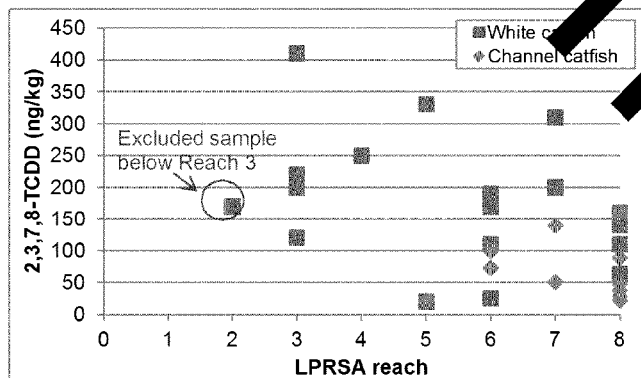


Figure 3-19. Catfish whole-body 2,3,7,8-TCDD concentrations by LPRSA reach

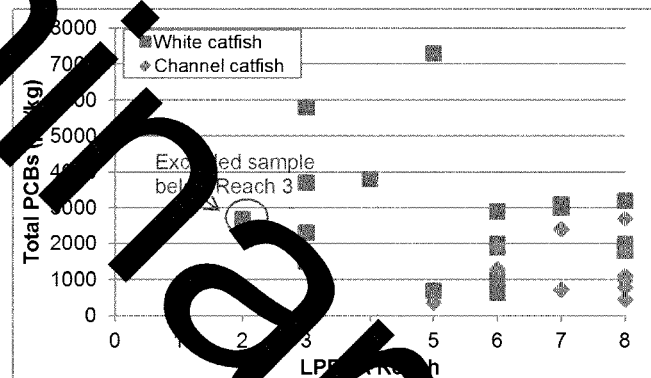
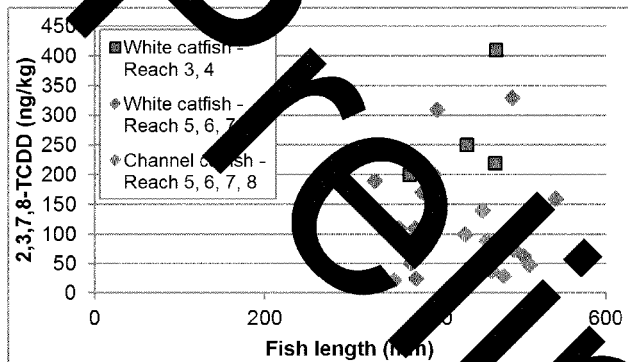
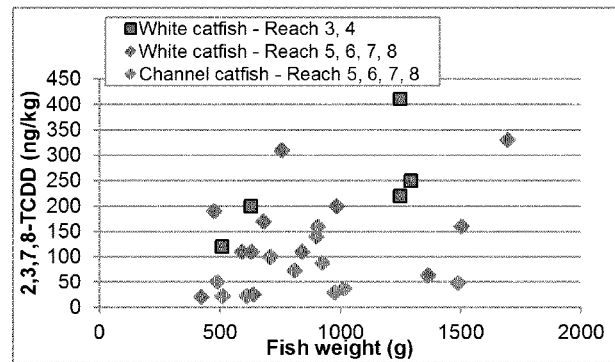


Figure 3-20. Catfish whole-body total PCB concentrations by LPRSA reach



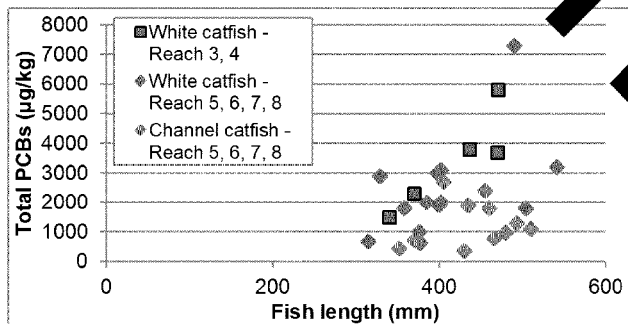
Note: Graph presents only catfish data included in calibration dataset.

**Figure 3-21. Catfish length and whole-body 2,3,7,8-TCDD concentrations**



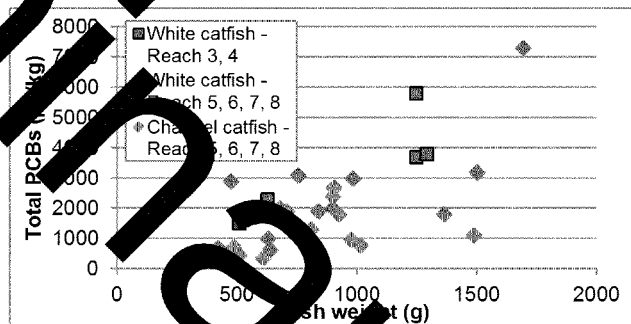
Note: Graph presents only catfish data included in calibration dataset.

**Figure 3-22. Catfish weight and whole-body 2,3,7,8-TCDD concentrations**



Note: Graph presents only catfish data included in calibration dataset.

**Figure 3-23. Catfish length and whole-body total PCB concentration**



Note: Graph presents only catfish data included in calibration dataset.

**Figure 3-24. Catfish weight and whole-body total PCB concentrations**

### 3.4 WHITE PERCH

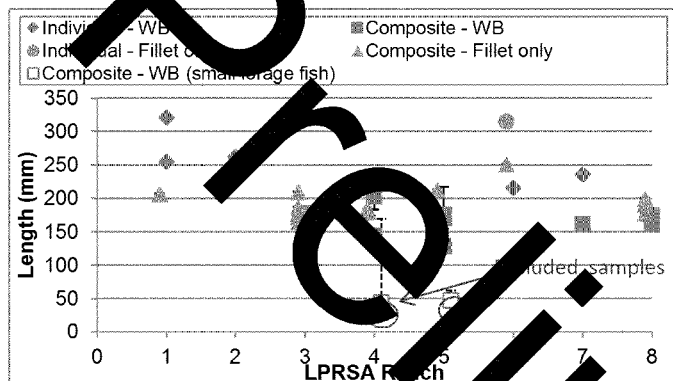
White perch (*Morone americana*) are included in the bioaccumulation model to represent invertivorous fish. White perch tissue data were analyzed as individual fish and fish composites for white perch collected from throughout the LPRSA; individual and composite samples were analyzed one of three ways:

- Fillet-only samples
- Fillet and carcass samples (analytical results were used to mathematically reconstitute whole-body concentrations)
- Whole-body samples

White perch analyzed as fillet-only samples were generally within the size range (in length and weight) of white perch analyzed as whole-body samples (Figures 3-25 and 3-26). Only white perch whole-body data were used in the bioaccumulation model calibration, although Figures 3-25 and 3-26 show fish sizes for fillet data for informational purposes. The two white perch samples analyzed as part of the 2010 small forage fish collection effort (Windward [in prep]-c) were not included in the white perch calibration dataset because these samples were based on white perch that were much smaller in size than the white perch collected in 2009 (Windward [in prep]-b) (see Figures 3-25 and 3-26). The white perch collected in 2009 are thought to better represent the size of perch caught and consumed by people; the creel / angler survey conducted along the LPRSA from 2010 to 2013 (ECOM [in prep]) reported that white perch collected for consumption (n=6) ranged in size from 165 to 180 mm.

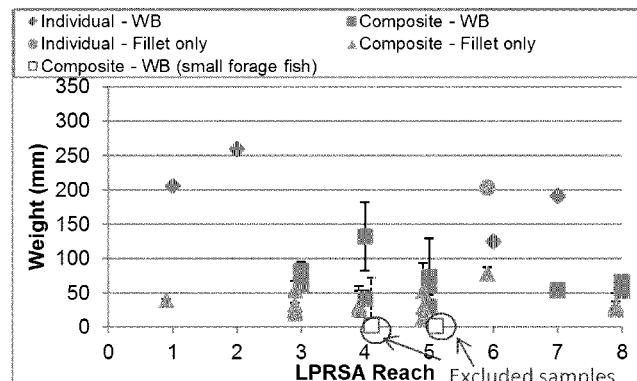
Whole-body data from both the whole-body samples and the reconstituted fillet and carcass samples were used in the bioaccumulation model. Figures 3-27 through 3-32 present white perch whole-body 2,3,7,8-TCDF and total PCB concentrations (excluding the two samples identified in Figures 3-25 and 3-26).

<sup>7</sup> Only one of the two white perch composite samples collected during the 2010 small forage fish sampling event was included in the small forage fish calibration dataset; the other sample was excluded given the wide range of fish sizes included in the composite sample (Section 4.2 of this attachment, which discusses the small forage fish dataset).



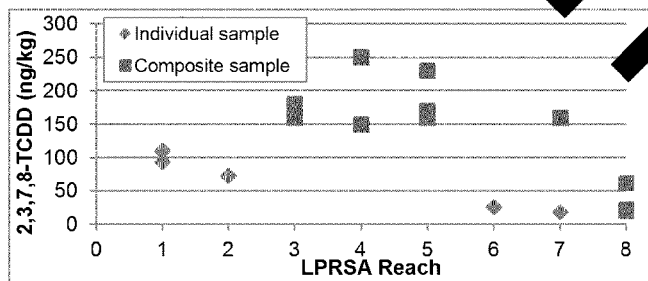
Note: Bars represent minimum and maximum values in composite sample. Fillet data are shown for informational purposes; only whole-body data collected in 2009 were used to calibrate the bioaccumulation model.

**Figure 3-25. Length of white perch in analytical samples by LPRSA reach**



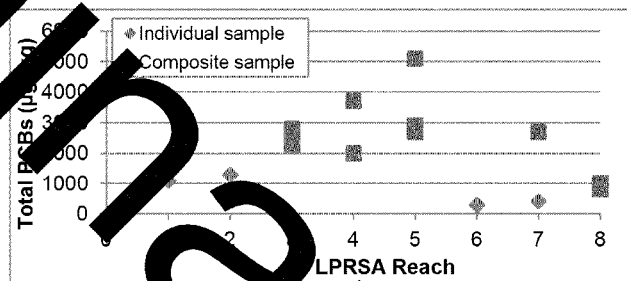
Note: Bars represent minimum and maximum values in composite sample. Fillet data are shown for informational purposes; only whole-body data collected in 2009 were used to calibrate the bioaccumulation model.

**Figure 3-26. Weight of white perch in analytical samples by LPRSA reach**



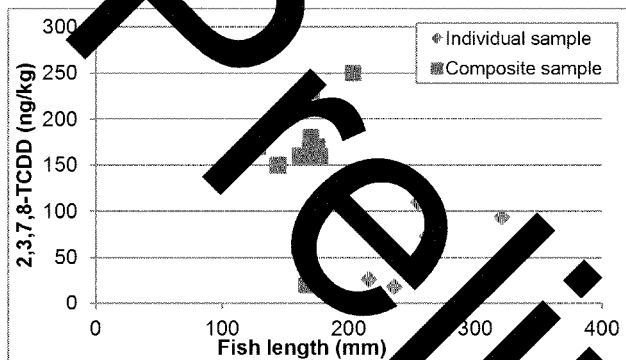
Note: Graph presents only white perch data included in calibration dataset.

**Figure 3-27. White perch whole-body 2,3,7,8-TCDD concentrations by LPRSA reach**



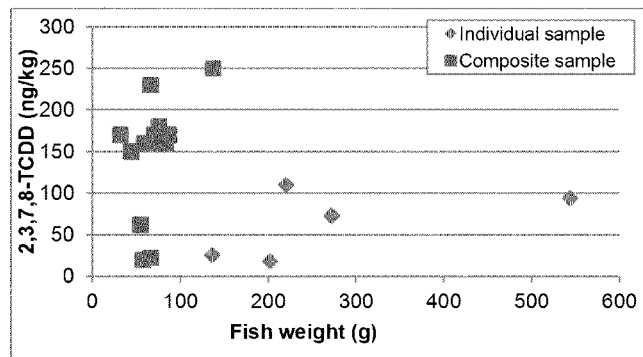
Note: Graph presents only white perch data included in calibration dataset.

**Figure 3-28. White perch whole-body total PCB concentrations by LPRSA reach**



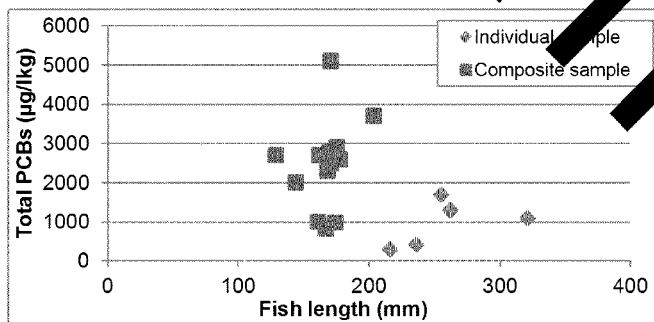
Note: Graph presents only white perch data included in calibration dataset.

**Figure 3-29. White perch length and whole-body 2,3,7,8-TCDD concentration**



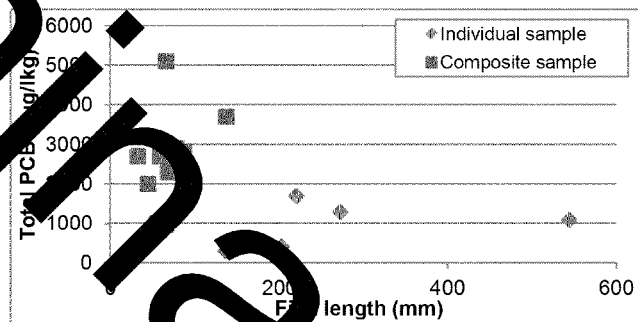
Note: Graph presents only white perch data included in calibration dataset.

**Figure 3-30. White perch weight and whole-body 2,3,7,8-TCDD concentrations**



Note: Graph presents only white perch data included in calibration dataset.

**Figure 3-31. White perch length and whole-body total PCB concentrations**



Note: Graph presents only white perch data included in calibration dataset.

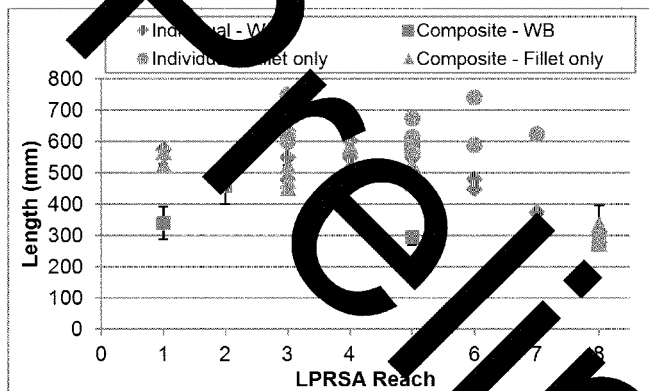
**Figure 3-32. White perch length and whole-body total PCB concentrations**

### 3.5 AMERICAN EEL

American eel (*Anguilla rostrata*) were included in the bioaccumulation model to represent piscivorous fish found throughout the LPRSA. Like white perch, American eel data were analyzed based on individual fish and fish composites collected from throughout the LPRSA; individual and composite samples were analyzed one of three ways:

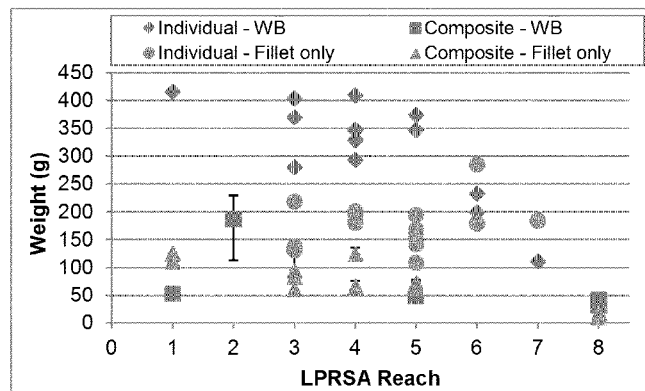
- Fillet-only samples
- Fillet and carcass samples (analytical results were used to mathematically reconstitute whole-body concentrations)
- Whole-body samples

American eel analyzed as fillet-only samples were generally similar in length but greater in weight than American eel analyzed as whole-body samples (Figures 3-33 and 3-34). Only American eel whole-body data were used in the bioaccumulation model calibration. Although Figures 3-33 and 3-34 show fish sizes for fillet data for informational purposes, whole-body data from both the whole-body samples and the reconstituted fillet and carcass samples were used in the bioaccumulation model. All available American eel whole-body data were used, regardless of eel size, although the dietary assumptions used in the bioaccumulation model were generally based on larger (e.g., > 50 cm) eel. The inclusion of all American eel size classes in the calibration dataset is discussed in the Uncertainty Analysis. Figures 3-35 through 3-40 present American eel whole-body 2,3,7,8-TCDF and total PCB concentrations.



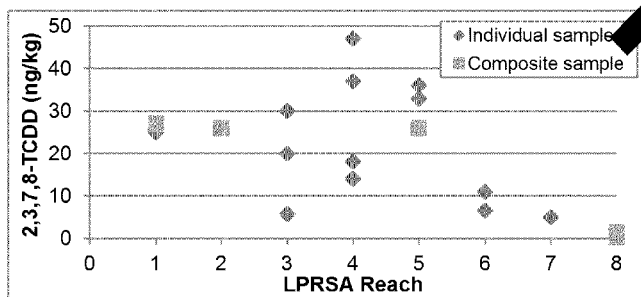
Note: Bars represent minimum and maximum values in composite sample. Fillet data are shown for informational purposes; only whole-body data were used to calibrate the bioaccumulation model.

**Figure 3-33. Length of American eel in analytical samples by LPRSA reach**



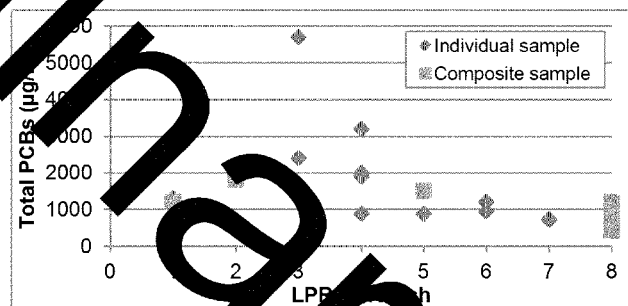
Note: Bars represent minimum and maximum values in composite sample. Fillet data are shown for informational purposes; only whole-body data were used to calibrate the bioaccumulation model.

**Figure 3-34. Weight of American eel in analytical samples by LPRSA reach**



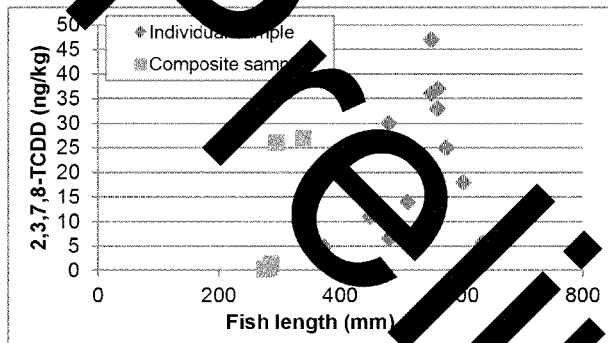
Note: All American eel whole-body data included in calibration dataset.

**Figure 3-35. American eel whole-body 2,3,7,8-TCDD concentrations by LPRSA reach**



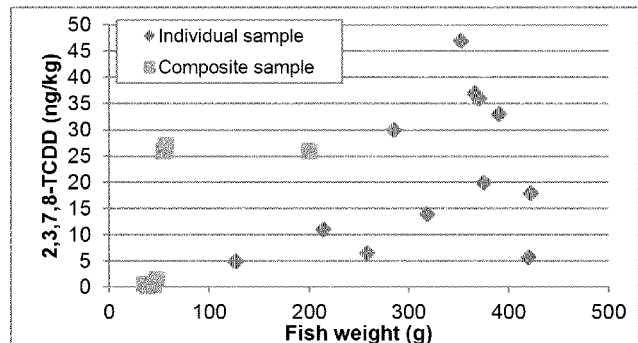
Note: All American eel whole-body data included in calibration dataset.

**Figure 3-36. American eel whole-body total PCB concentrations by LPRSA reach**



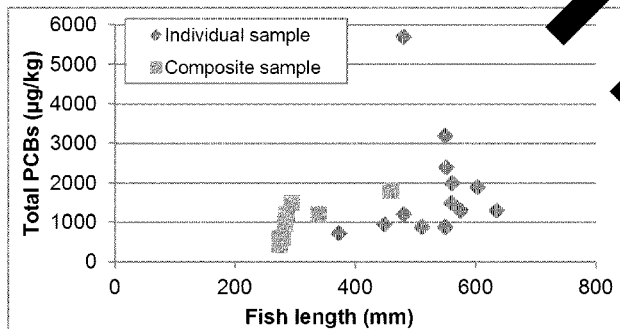
Note: All American eel whole-body data included in calibration dataset.

**Figure 3-37. American eel length and whole-body 2,3,7,8-TCDD concentration**



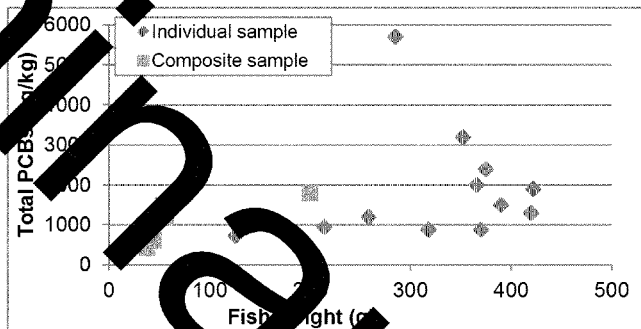
Note: All American eel whole-body data included in calibration dataset.

**Figure 3-38. American eel weight and whole-body 2,3,7,8-TCDD concentrations**



Note: All American eel whole-body data included in calibration dataset.

**Figure 3-39. American eel length and whole-body total PCB concentrations**



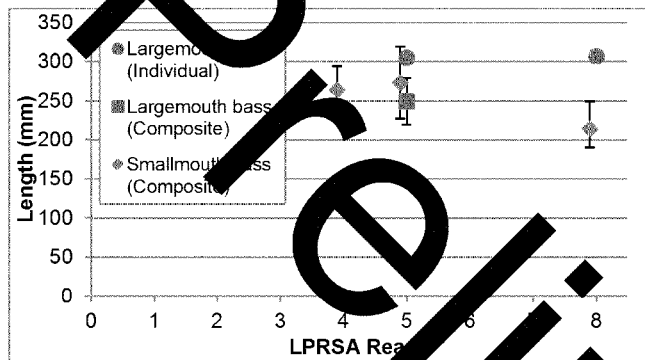
Note: All American eel whole-body data included in calibration dataset.

**Figure 3-40. American eel weight and whole-body total PCB concentrations**

### 3.6 FRESHWATER BASS

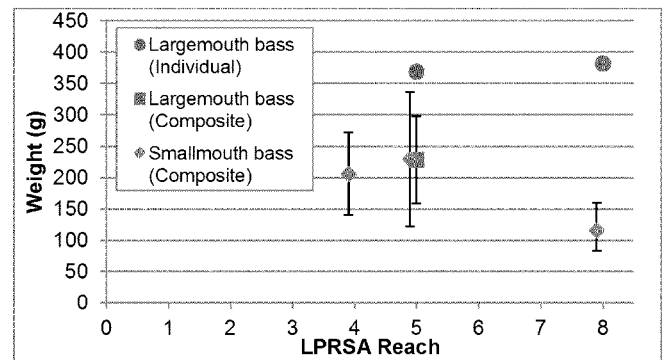
The freshwater bass compartment of the bioaccumulation model includes both smallmouth bass (*Micropterus dolomieu*) and largemouth bass (*Micropterus salmoides*). Smallmouth and largemouth bass have similar life histories and diets. Both are opportunistic feeders and primarily feed on small fish and invertebrates based on prey availability (George and Hadley 1979; Turner 1966a; Wydoski and Whitney 1979). Smallmouth and largemouth bass collected in the LPRSA for analysis were generally similar in size (Figures 3-41 and 3-42). Both were limited to the upper portion (above RM 6) of the LPRSA.

Available smallmouth and largemouth bass whole-body data were evaluated in the bioaccumulation model calibration; however, data were limited to three smallmouth and three largemouth bass whole-body samples. Freshwater bass whole-body (both fillet and carcass tissue) data were based on the analysis of individual fish or fish composites composed of two or three fish). Whole-body concentrations that were mathematically constituted based on the fillet and carcass weights and concentrations were used in the bioaccumulation model. Figures 3-43 through 3-48 present the whole-body bass 15,7,8-TBDD and total PCB concentrations.



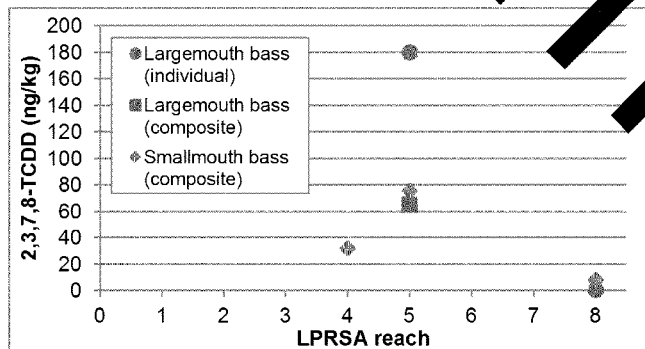
Note: Bars represent minimum and maximum values in composite sample.

**Figure 3-41. Length of freshwater bass in analytical samples by LPRSA reach**



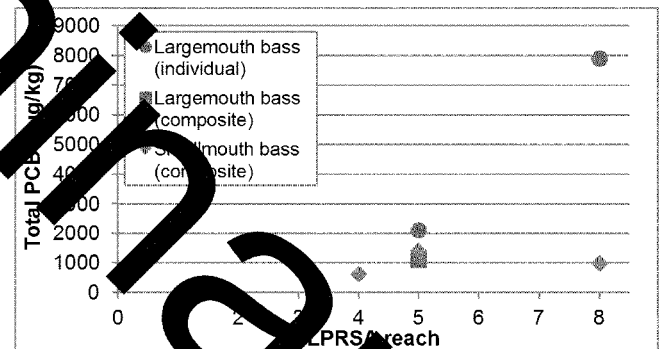
Note: Bars represent minimum and maximum values in composite sample.

**Figure 3-42. Weight of freshwater bass in analytical samples by LPRSA reach**



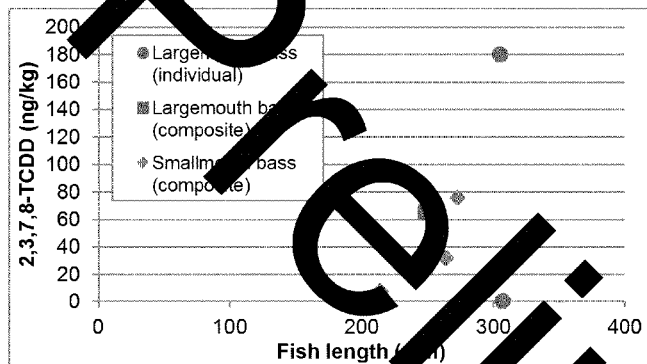
Note: All freshwater bass whole-body data included in calibration dataset.

**Figure 3-43. Freshwater bass whole-body 2,3,7,8-TCDD concentrations by LPRSA reach**



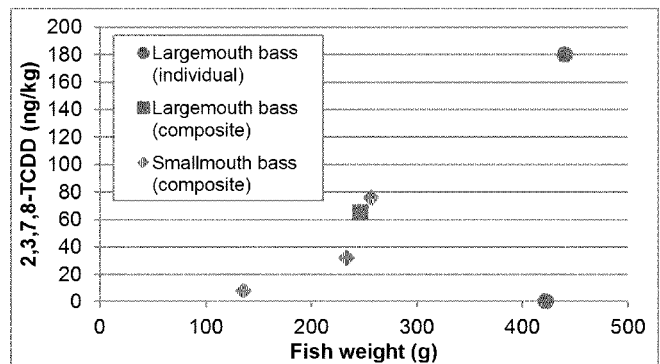
Note: All freshwater bass whole-body data included in calibration dataset.

**Figure 3-44. Freshwater bass whole-body total PCB concentrations by LPRSA reach**



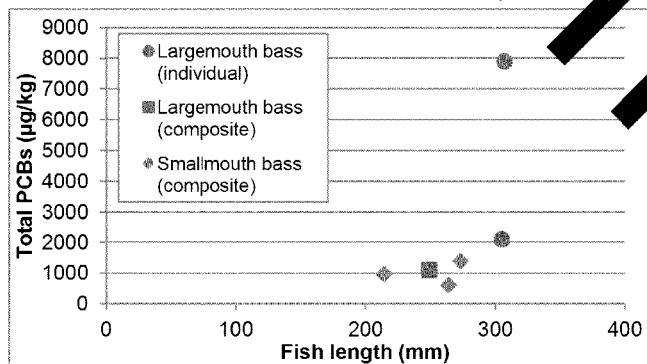
Note: All freshwater bass whole-body data included in calibration dataset.

**Figure 3-45. Freshwater bass length and whole-body 2,3,7,8-TCDD concentration**



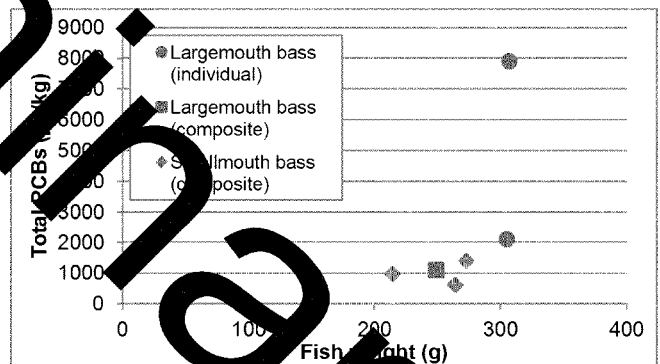
Note: All freshwater bass whole-body data included in calibration dataset.

**Figure 3-46. Freshwater bass weight and whole-body 2,3,7,8-TCDD concentrations**



Note: All freshwater bass whole-body data included in calibration dataset.

**Figure 3-47. Freshwater bass length and whole-body total PCB concentrations**



Note: All freshwater bass whole-body data included in calibration dataset.

**Figure 3-48. Freshwater bass weight and whole-body total PCB concentrations**

## 4 Additional Data Evaluated in the Bioaccumulation Model

Tables 4-1 and 4-2 summarize the whole-body data available for additional fish species and invertebrates that were not used to calibrate the bioaccumulation model because they were not target species or lacked sufficient current LPRSA data for calibration. These data were evaluated in the uncertainty analysis of the bioaccumulation model. Details regarding these data and their sources are provided in Sections 4.1 to 4.4.

**Table 4-1. Summary of tissue samples for additional fish and invertebrate species evaluated in the bioaccumulation model uncertainty analysis**

LPRSA Segment	Number of Whole-Body Samples													
	Filter-Feeding Fish <sup>a</sup>		Small Forage Fish <sup>b</sup>		Brown Bullhead		White Sucker		Northern Pike		Benthic C/O <sup>c</sup>		Benthic DEP <sup>d</sup>	
	C	I	C	I	C	I	C	I	C	I	C	I	C	I
RM 0 – RM 2 (Reach 1)	3	-	2	-	-	-	-	-	-	-	3	-	-	-
RM 2 – RM 4 (Reach 2)	-	-	6	-	-	-	-	-	-	-	1	-	-	-
RM 4 – RM 6 (Reach 3)	3	-	3	-	-	1	-	-	-	-	1	-	-	-
RM 6 – RM 8 (Reach 4)	1	-	-	-	-	1	-	1	-	-	-	-	3	-
RM 8 – RM 10 (Reach 5)	-	-	4	-	-	-	-	2	-	-	-	-	3	-
RM 10 – RM 12 (Reach 6)	-	-	2	-	3	-	-	-	1	-	-	-	2	-
RM 12 – RM 14 (Reach 7)	1	-	-	-	-	1	-	-	-	-	-	-	5	-
RM 14 – RM 17.4 (Reach 8)	-	-	-	-	-	-	-	2	-	-	-	-	1	-
<b>Site-wide total</b>	<b>9</b>	<b>0</b>	<b>25</b>	<b>0</b>	<b>6</b>	<b>0</b>	<b>5</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>5</b>	<b>0</b>	<b>14</b>	<b>0</b>
	<b>9</b>		<b>25</b>						<b>1</b>		<b>5</b>		<b>14</b>	

<sup>a</sup> Filter-feeding fish includes small gizzard shad (n = 3) data.

<sup>b</sup> Small forage fish includes mummichog (n = 18), white perch (n = 1), silver shiner (n = 1), spottail shiner (n = 1), and mixed forage fish (n = 4) data.

<sup>c</sup> Estuarine worm (*Nereis virens*) laboratory bioaccumulation tissue data.

<sup>d</sup> Freshwater worm (*Lumbriculus variegatus*) laboratory bioaccumulation tissue data.

C – composite sample

C/O – carnivore/omnivore

DEP – deposit feeder

I – individual fish sample

LPRSA – Lower Potomac River Study Area

RM – river mile

**Table 4-2. Summary of empirical concentrations for additional tissue evaluated in the bioaccumulation model uncertainty analysis**

Species	Modeling Area	No. of Samples	Concentration <sup>a</sup>					
			2,3,7,8-TCDD (ng/kg ww)		Tetrachlorobiphenyl (µg/kg ww)		Total PCB Congeners (µg/kg ww)	
			Mean	SD	Mean	SD	Mean	SD
Filter-feeding fish <sup>b</sup>	site-wide <sup>c</sup>	3	30	17	120	40	380	120
Small forage fish <sup>b</sup>	site-wide	25	37	26	120	55	510	200
Brown bullhead	RM 4-17.4	6	91	71	190	160	870	610
White sucker	RM 6-17.4	5	59	53	260	140	1,500	910
Northern pike	RM 6-17.4	1	95	na	430	na	2,000	na
Benthic C/O <sup>d</sup>	site-wide <sup>e</sup>	5	6.1	7.3	15	16	53	43
Benthic DEP <sup>f</sup>	RM 6-17.4	14	27	37	51	48	180	160

- <sup>a</sup> Based on collected concentrations of tissue.
- <sup>b</sup> Filter-feeding fish includes young-of-the-year Atlantic menhaden and small gizzard shad data; only LPRSA gizzard shad data were available.
- <sup>b</sup> Small forage fish includes northern pike (n = 18), white perch (1 sample), silver shiner (n = 1), and spottail shiner (n = 1), and mixed forage fish (n = 4) data.
- <sup>c</sup> Samples were available only between RM 6 and RM 14 (Reaches 4 through 7).
- <sup>d</sup> Estuarine worm (*Nereis virens*) laboratory bioaccumulation tissue data.
- <sup>e</sup> Samples were available only between RM 0 and RM 6 (Reaches 1 through 3).
- <sup>f</sup> Freshwater worm (*Lumbriculus variegatus*) laboratory bioaccumulation tissue data.
- C/O – carnivore/omnivore  
DEP – deposit feeder  
LPRSA – Lower Passaic River Study Area  
na – not applicable  
PCB – polychlorinated biphenyl
- RM – river mile  
SD – standard deviation  
TCDD – tetrachlorodibenzo-*p*-dioxin  
ww – wet weight

#### 4.1 SMALL FILTER-FEEDING FISH

The small filter-feeding fish compartment of the bioaccumulation model includes juvenile (young-of-the-year) Atlantic menhaden (*Brevoortia tyrannus*) and small gizzard shad (*Dorosoma cepedianum*).

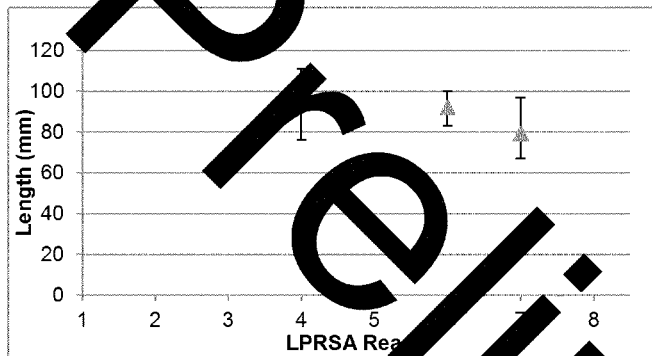
Limited LPRSA data were available for filter-feeding fish; these were highly composite samples were collected during the 2010 small forage fish sampling effort (Windward [in prep]-c). LPRSA data were available for adult Atlantic menhaden, but not for juvenile Atlantic menhaden. Because current data were limited, filter-feeding fish data were not used in the calibration of the bioaccumulation model. Gizzard shad data were evaluated as part of the uncertainty assessment of the bioaccumulation model to estimate how well small filter-feeding tissue concentrations were estimated.

Figures 4-1 and 4-2 present data on the mean length and weight, respectively, of fish analyzed in the gizzard shad composite samples; individual fish ranged from 67 to 111 mm in length. Juvenile Atlantic menhaden data for the LPRSA were not available; however, in the general literature, juvenile Atlantic menhaden have been reported to

range from 55 to 140 mm in length (Rogers and van den Avyle 1989), which is similar to the lengths of collected LPRSA gizzard shad. Figures 4-3 and 4-4 present gizzard shad 2,3,7,8-TCDD and total PCB concentrations. Adult Atlantic menhaden data<sup>8</sup> for total PCBs and 2,3,7,8-TCDD from the LPRSA 1999 sampling effort conducted by TCEQ were available (BBL 2001); however, these fish were not expected to represent the size of fish consumed by higher trophic levels.

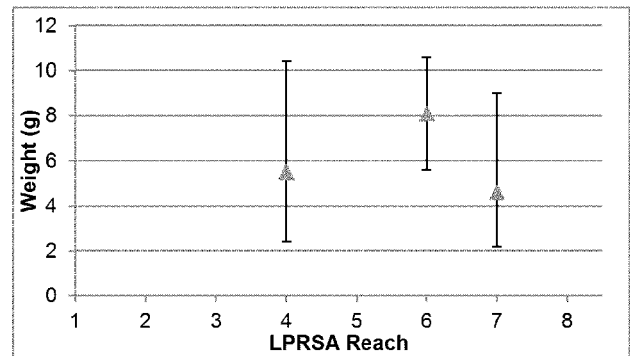
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<sup>8</sup> Atlantic menhaden caught during the 1999 sampling effort at LPRSA locations were an average of 342 mm long in Reach 1 and 304 mm long in Reach 3 (BBL 2001). Atlantic menhaden caught from the LPRSA during the 2009 and 2010 fish community surveys (n = 149 fish with reported size data) ranged from 80 to 390 mm in size; only three of the fish were < 270 mm.



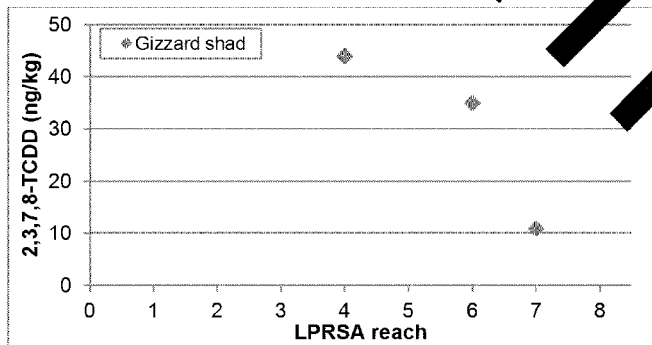
Note: Bars represent minimum and maximum values in composite sample.

**Figure 4-1. Mean length of gizzard shad in analytical composite samples**

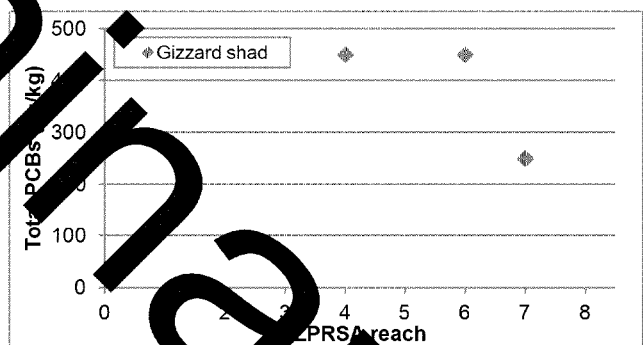


Note: Bars represent minimum and maximum values in composite sample.

**Figure 4-2. Mean weight of gizzard shad in analytical composite samples**



**Figure 4-3. Gizzard shad whole-body 2,3,7,8-TCDD concentrations by LPRSA reach**



**Figure 4-4. Gizzard shad whole-body total PCB concentrations by LPRSA reach**

## 4.2 SMALL FORAGE FISH

The small forage fish compartment of the bioaccumulation model includes primarily muskellunge (*Fundulus heteroclitus*), but it also includes other species, such as shiners (*Notropis* spp.), striped mullet (*Mugil cephalus*), and tessellated darter (*Etheostoma blennioides*). Composite samples of small forage fish were analyzed for a number of species: muskellunge (n = 18), gizzard shad (n = 3), pumpkinseed (n = 1), silver shiner (n = 1), spottail shiner (n = 1), white perch (n = 2), and mixed forage fish composites (n = 4). Mixed forage fish samples were composed of multiple small forage fish species (Table 4-3).

**Table 4-3. Composition of mixed forage fish samples**

Sample ID	No. of Fish in Sample	Reach	RM	Fish Species
LPR4-MXWB-Comp01	4	4	3.0	smallmouth bass (n = 1), striped bass (n = 2), tessellated darter (n = 4), striped mullet (n = 2), gizzard shad (n = 10), spottail shiner (n = 6), and Atlantic silverside (n = 1)
LPR5-MXWB-Comp02	5	5	8.4	striped mullet (n = 1), white perch (n = 45), gizzard shad (n = 15), spottail shiner (n = 7), and inland silverside (n = 1)
LPR6-MXWB-Comp03	74	74	11.2	striped bass (n = 5), bluegill (n = 9), striped mullet (n = 5), white perch (n = 48), and Atlantic silverside (n = 7)
LPR8-MXWB-Comp04	18	8	1	smallmouth bass (n = 2), striped bass (n = 1), gizzard shad (n = 4), and inland silverside (n = 11)

ID – identification

RM – river mile

The small forage fish data used to calibrate the bioaccumulation model included only those fish samples that represented fish small enough to be preyed upon by other LPRSA fish and that were generally benthic feeding fish. Gizzard shad, although collected under the 2010 small forage fish sampling effort (Windward 2011), were excluded from the bioaccumulation calibration dataset for small forage fish because this species is more representative of filter-feeding fish, which were modeled as a separate compartment in the bioaccumulation model (see Section 4.1 for discussion of filter-feeding fish data). In addition, larger fish collected during the 2010 small forage fish sampling effort that did not represent appropriate prey for modeled LPRSA fish-eating fish were not included in the calibration dataset for small forage fish (Figures 4-5 and 4-6). Such samples included the single pumpkinseed composite sample<sup>9</sup> (composed of three fish ranging from 141 to 150 mm in length) and one of two

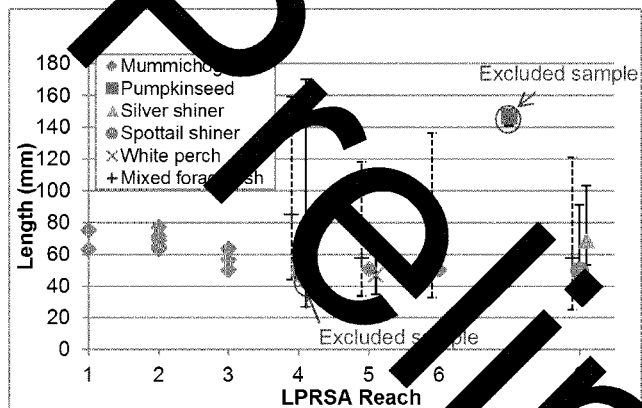
<sup>9</sup> The 2,3,7,8-TCDD and total PCB concentrations in the pumpkinseed sample excluded from the calibration dataset were 7.5 and 170 µg / kg, respectively.

white perch samples<sup>10</sup> that included 1 large fish (170 mm in length) and 120 smaller fish (ranging from 27 to 57 mm in length). Figures 4-7 through 4-12 present small forage fish 2,3,7,8-TCDD and total PCB concentrations (excluding the two samples identified in Figures 4-5 and 4-6).

There is some uncertainty associated with the inclusion of the four mixed forage fish samples in the small forage fish calibration dataset, because a portion of these samples was made up of fish species (e.g., gizzard shad) that may be more representative of filter-feeding fish<sup>11</sup> than small forage fish. This uncertainty was considered in the evaluation of model calibration results, although 2,3,7,8-TCDD and total PCBs concentrations in mixed forage fish samples are within the range of those in the other small forage fish samples (Figure 4-7 through 4-12).

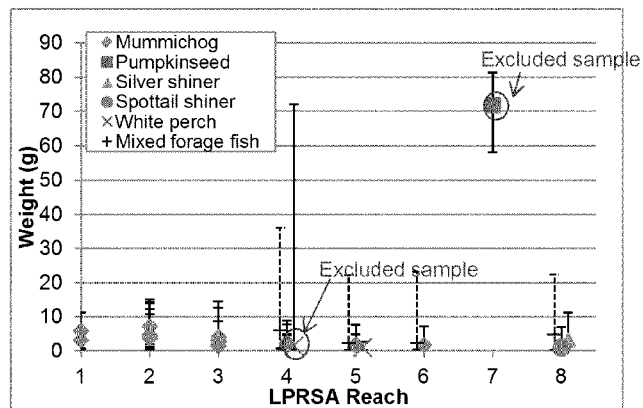
<sup>10</sup> The 2,3,7,8-TCDD and total PCB concentrations in the white perch sample excluded from the calibration dataset were 160 and 1,800 µg / kg, respectively.

<sup>11</sup> Filter-feeding fish were modeled as a separate compartment in the bioaccumulation model.



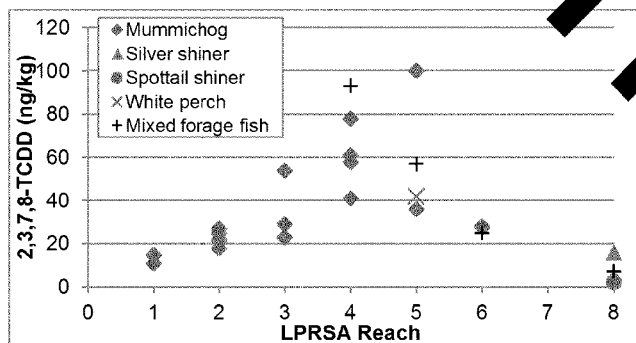
Note: Bars represent minimum and maximum values in composite sample.

**Figure 4-5. Mean length of small forage fish in analytical samples by LPRSA reach**



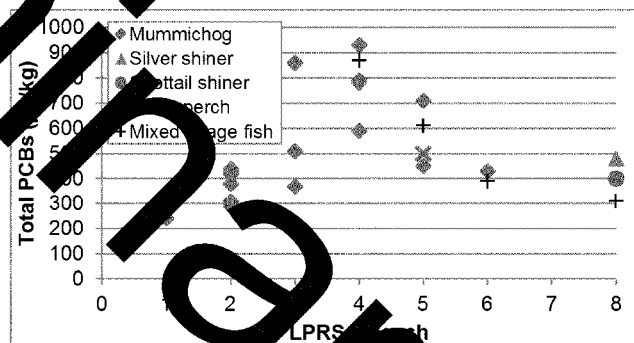
Note: Bars represent minimum and maximum values in composite sample.

**Figure 4-6. Mean weight of small forage fish in analytical samples by LPRSA reach**



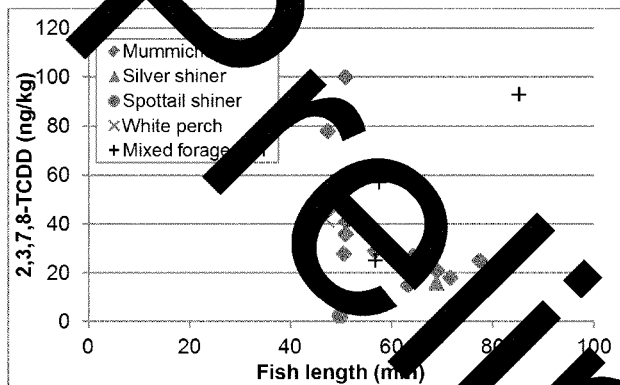
Note: Graph presents only small forage fish included in calibration dataset.

**Figure 4-7. Small forage fish 2,3,7,8-TCDD concentrations by LPRSA reach**



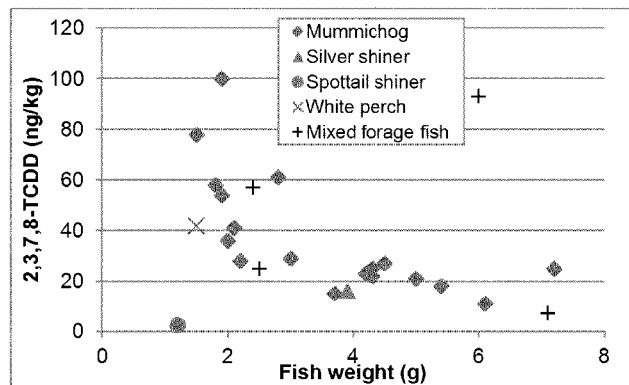
Note: Graph presents only small forage fish included in calibration dataset.

**Figure 4-8. Small forage fish total PCB concentrations by LPRSA reach**



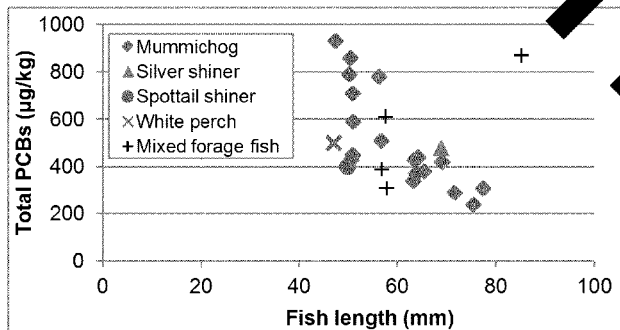
Note: Graph presents only small forage fish included in calibration dataset.

**Figure 4-9. Small forage fish average composite length and 2,3,7,8-TCDD concentration**



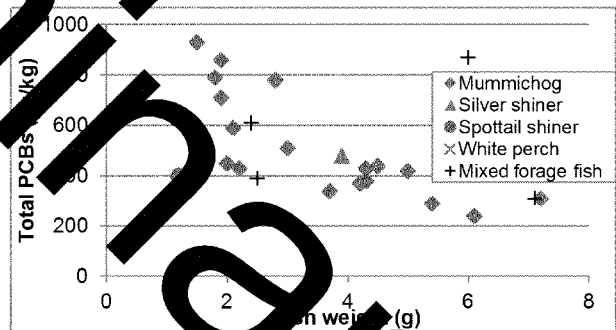
Note: Graph presents only small forage fish included in calibration dataset.

**Figure 4-10. Small forage fish average composite weight and 2,3,7,8-TCDD concentrations**



Note: Graph presents only small forage fish included in calibration dataset.

**Figure 4-11. Small forage fish average composite length and total PCB concentrations**



Note: Graph presents only small forage fish included in calibration dataset.

**Figure 4-12. Small forage fish average composite weight and total PCB concentrations**

### 4.3 OTHER FISH SPECIES

Whole-body tissue data from the LPRSA 2009 tissue collection effort (Windward [in press b]) were available for three additional fish species not explicitly modeled in the bioaccumulation model:

- Brown bullhead
- White sucker
- Northern pike

Whole-body data for these fish were based on the analysis of both fillet and carcass tissue from individual fish. Whole-body concentrations were mathematically reconstituted based on the fillet and carcass weights and concentrations. Figures 4-13 and 4-14 present data on the sizes of these other fish species. Figures 4-15 through 4-20 present concentrations of 2,3,7,8-CDD and total PCB for these other fish species.

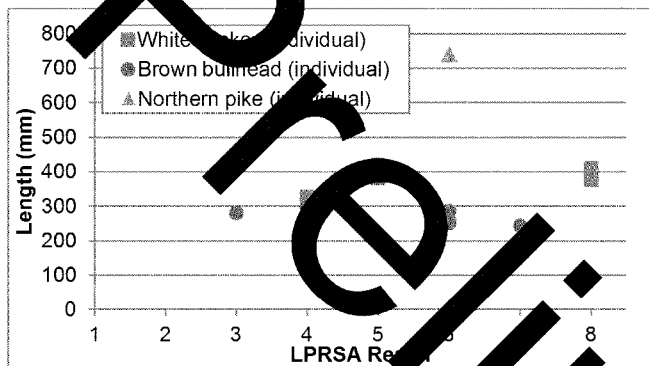


Figure 4-13. Length of other fish species in analytical samples by LPRSA reach

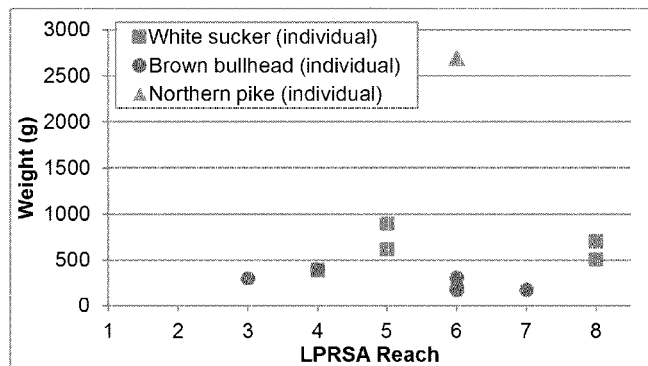


Figure 4-14. Weight of other fish species in analytical samples by LPRSA reach

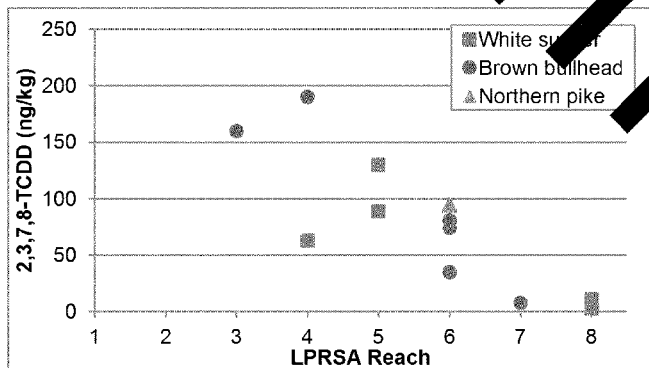


Figure 4-15. Other fish species whole-body 2,3,7,8-TCDD concentrations by LPRSA reach

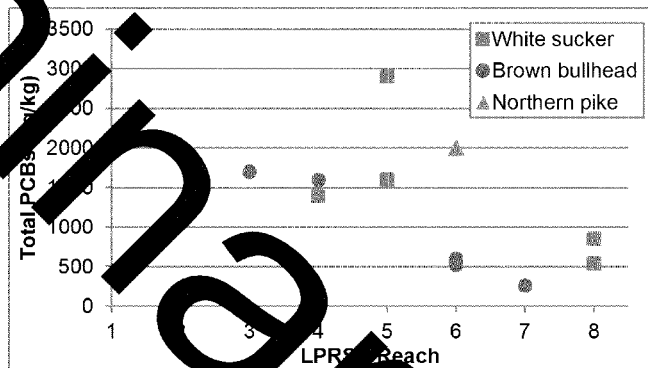


Figure 4-16. Other fish species whole-body total PCB concentrations by LPRSA reach

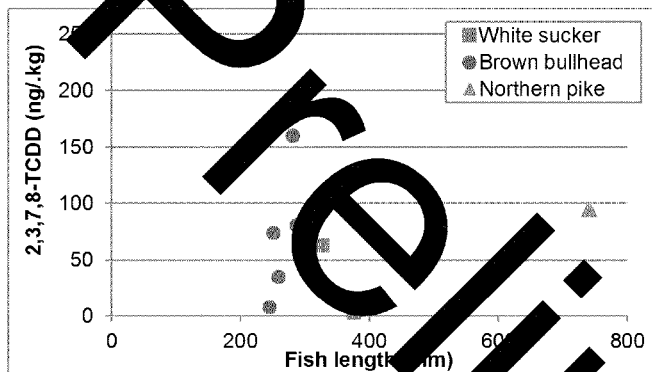


Figure 4-17. Other fish species length and whole-body 2,3,7,8-TCDD concentrations

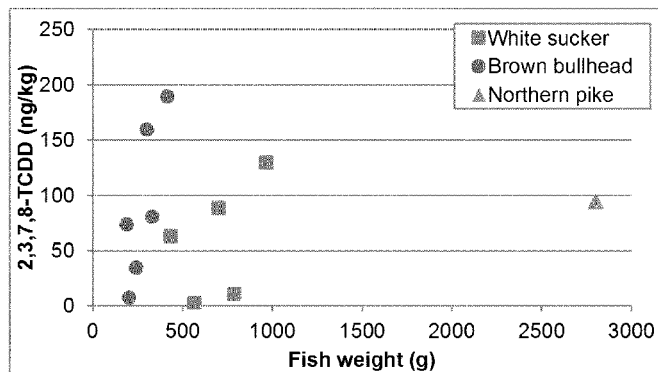


Figure 4-18. Other fish species weight and whole-body 2,3,7,8-TCDD concentrations

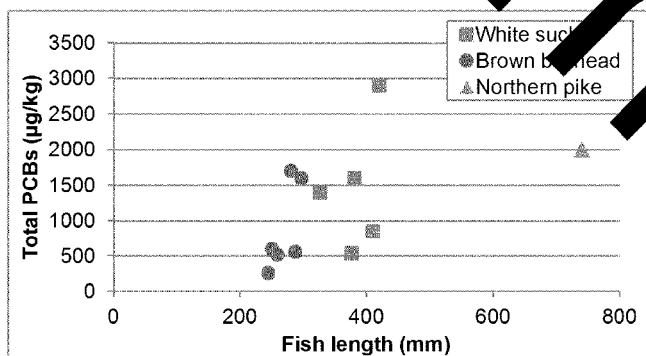


Figure 4-19. Other fish species length and whole-body total PCB concentrations

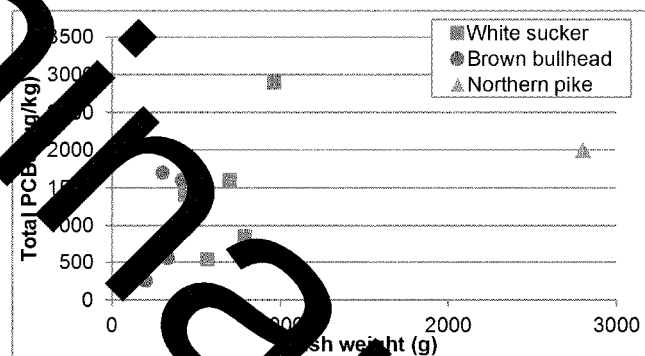


Figure 4-20. Other fish species weight and whole-body total PCB concentrations

#### 4.4 BENTHIC INVERTEBRATE BIOACCUMULATION TISSUE

Benthic invertebrate tissue data from laboratory bioaccumulation tests based on LPEA surface sediment collected in 2009 (Windward [in prep]-a) were available for:

- Estuarine worm (*Nereis virens*)
- Freshwater worm (*Lumbriculus variegatus*)

Current bioaccumulation tissue data were evaluated as part of the uncertainty assessment of the bioaccumulation model. Estuarine and freshwater worm data were compared to the modeled benthic invertebrate carnivore/omnivore (C/O) and benthic invertebrate deposit feeder (DEP) compartments, respectively, based on the feeding habits of these species. *L. variegatus*, a head-down deposit feeder that can grow to be fairly large (generally as much as 9 mg wet weight [ww]) (Williams 2005; Vieira et al. 2006), was characterized as a benthic invertebrate DEP. *N. virens* was characterized as a benthic invertebrate C/O because it is a predatory carnivore; this estuarine worm can grow as large as 15 cm in length but is generally 1 to 5 cm long (Kristensen 1984; Caron and Desrosiers 2004). Figures 4-21 and 4-22 present bioaccumulation invertebrate 2,3,7,8-TCDD and total PCB concentrations.

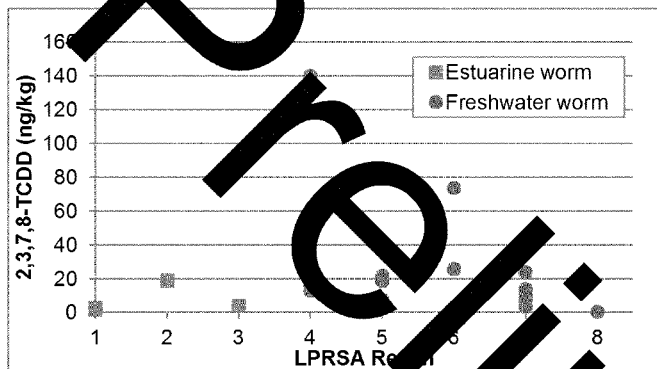


Figure 4-21. Benthic invertebrate bioaccumulation tissue 2,3,7,8-TCDD concentrations by LPRSA reach

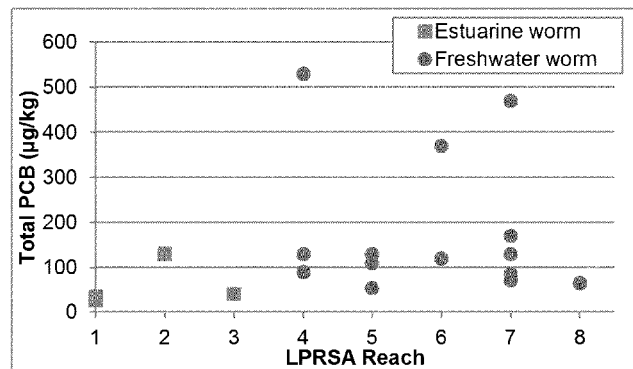


Figure 4-22. Benthic invertebrate bioaccumulation tissue total PCB concentrations by LPRSA reach

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## ATTACHMENT 2. USE OF CFT MODEL DATA FOR CALIBRATION

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Preliminary

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## 1 Description of CFT Model Output

This attachment describes how the contaminant fate and transport (CFT) model output was summarized for use in the bioaccumulation model. Data from the CFT model were provided to Windward Environmental LLC (Windward) on October 31, 2014 (with updates provided on January 14, 2015, and March 2, 2015), for use in the calibration of the bioaccumulation model. The following provides details regarding the CFT model output that was used to calibrate the bioaccumulation model:

- Data included monthly average values for three years of model output (October 2012 to September 2013).
- Values were provided for a total of 26 spatial areas (13 spatial segments for both river-wide and mudflat-only areas). The three spatial scales that were directly used for model calibration were site wide, river mile (RM) 4 to Dundee Dam, and RM 7 to Dundee Dam. Both river-wide (i.e., bank-to-bank) and mudflat-only values were used based on the selected modeling area for fish.
- Model runs were provided for two chemicals (2,3,7,8-tetrachlorodibenzo-*p*-dioxin (TCDD) and tetraCB)
- CFT model output included nine parameters (including five that were chemical specific) that were used as inputs for the bioaccumulation model. These included chemical concentration, water temperature, and organic carbon content (Table 1-1).

Table 1-1 provides a summary of the nine parameters derived from the CFT model output that were used to calibrate the bioaccumulation model.

**Table 1-1. Bioaccumulation model parameters derived from CFT model output**

Parameter Name	Model Code	Units	Notes
<b>Chemical-Specific Parameters</b>			
Chemical concentration in sediment	CST	ng/g dw	top 2-cm layer; area-weighted average
Chemical concentration in porewater	CSD	ng/g	area-weighted average
Chemical concentration in bioavailable water	CWB	ng/g	volume-weighted average
Chemical concentration in water column particulates	CPART	ng/g dw	volume-weighted average
Chemical concentration in near-bottom particulates	CPART_DET	ng/g dw	area-weighted average
<b>Non-Chemical-Specific Parameters</b>			
Mean water temperature	TW	°C	area-weighted average
OC content of sediment	OCSS	fraction	top 2-cm layer; area-weighted average
OC content of water column particulates	OCPART	fraction	volume-weighted average
OC content of near-bottom particulates (fluff layer)	OCPART_DET	fraction	area-weighted average

CFT – contaminant fate and transport

The following describes the averaging of the CFT model output for the various parameters:

- **Daily averages** – Averages for each day were provided for each parameter.
- **Spatial resolution** – The Lower Passaic River Study Area (LPRSA) CFT model is divided into cells, each of which is modeled individually. Cells are averaged by area or volume (depending on the parameter, as noted in Table 1-1) to obtain values for larger areas (e.g., RM 4 to 17.4) evaluated in the bioaccumulation model.
- **Water column depth layers** – A total of 10 layers are used to model the water column. Each layer consists of 10% of the water column depth in a given cell.
- **Sediment bed depth layers** – As with the water column, the bedded sediment is modeled in layers. The depth of the top layer is variable, ranging from 0.5 to 2 cm. After the first layer, each subsequent layer has a depth of 1 cm. The bioaccumulation model uses the top two sediment bed depth layers.

Table 1-2 lists the CFT model parameters used to calculate the bioaccumulation model parameters presented in Table 1-1. Table 1-3 presents the equations used to convert the CFT model parameters to those needed for the bioaccumulation model.

**Table 1-2. Definition of CFT model parameters**

Parameter	Parameter Description
TW	water temperature (°C)
C <sub>wc,diss,1-10</sub>	depth-average dissolved concentration in water column
DOC <sub>wc</sub>	dissolved organic carbon concentration in water column
K <sub>ow</sub>	octanol-water partitioning coefficient
C <sub>wc,part,1-10</sub>	depth-average concentration in particulates in water column
TSS <sub>wc,1-10</sub>	depth-average concentration of suspended solids in water column
POC <sub>wc,1-10</sub>	depth-average particulate organic carbon concentration in water column
POC <sub>wc,10</sub>	particulate organic carbon concentration in bottom layer of water column
C <sub>wc,part,10</sub>	concentration in particulates in bottom layer of water column (near-bottom particulates)
TSS <sub>wc,10</sub>	concentration of suspended solids in bottom layer of water column
C <sub>bed,diss,1-X</sub>	depth-average dissolved concentration in sediment bed between layers 1 and X
Φ	porosity
TSS <sub>bed,1-X</sub>	depth-average concentration of suspended solids in sediment bed between layers 1 and X
ρ <sub>water</sub>	specific gravity of water (constant equal to 1 <sup>a</sup> )
C <sub>bed,part,1-X</sub>	depth-average concentration in particulates in sediment bed between layers 1 and X
POC <sub>bed,1-X</sub>	depth-average organic carbon concentration in particulates in sediment bed between layers 1 and X

<sup>a</sup> Values for these constants are current as of February 18, 2015.

CFT – contaminant fate and transport

DOC – dissolved organic carbon

TSS – total suspended solids

POC – particulate organic carbon

**Table 1-3. Equations used to calculate bioaccumulation model parameters from CFT model parameters**

Bioaccumulation Model Parameter		Equation from CFT Parameters <sup>a</sup>
Model Code	Name	
Chemical-specific parameters		
CST	Chemical concentration in sediment	= C <sub>bed,part,1-X</sub> / TSS <sub>bed,1-X</sub>
CSD	Chemical concentration in porewater	= C <sub>bed,diss,1-X</sub> / ρ <sub>water</sub>
CWB	Chemical concentration in bioavailable water	= C <sub>wc,diss,1-10</sub> / (1 + K <sub>ow</sub> x ADOC x DOC <sub>wc</sub> )
CPART	Chemical concentration in water column particulates	= C <sub>wc,part,1-10</sub> / TSS <sub>wc,1-10</sub>
CPART_DET	Chemical concentration in near-bottom particulates	= C <sub>wc,part,10</sub> / TSS <sub>wc,10</sub>
Non-chemical-specific parameters		
TW	Mean water temperature	= TW
OC <sub>bed</sub>	Organic content of sediment	= POC <sub>bed,1-X</sub> / TSS <sub>bed,1-X</sub>
OCPART	Organic content of water column particulates	= POC <sub>wc,1-10</sub> / TSS <sub>wc,1-10</sub>
OCPART_DET	Organic content of near-bottom particulates (fluff layer)	= POC <sub>wc,10</sub> / TSS <sub>wc,10</sub>

<sup>a</sup> The second term in the subscript designates the CFT model layer(s) (water column or sediment bed) included in the calculation.

ADOC – DOC proportionality constant (Arar and Gobas 2004)

CFT – contaminant fate and transport

## 2 Summary of Data Used in Bioaccumulation Model Calibration

CFT model output was averaged over the calibration period (i.e., the three years for which data were provided) to develop input estimates for the steady state model. The average values used in model calibration for each parameter (and spatial segment) are presented in Table 2-1 and 2-2 for chemical-specific parameters and Table 2-3 for non-chemical-specific parameters. Additionally, minimum and maximum values for each parameter are presented to indicate the range of values in the calibration dataset.

**Table 2-1 Chemical-specific parameter values for 2,3,7,8-TCDD**

Parameter Name	Unit	Spatial Segment	River-wide Parameter Values for 2,3,7,8-TCDD			Mudflats-only Parameter Values for 2,3,7,8-TCDD		
			Average	Minimum	Maximum	Average	Minimum	Maximum
Concentration in sediment solids (CST)	ng/g dw	site wide	0.46	0.36	0.78	0.37	0.18	0.75
		RM 4-DD	0.58	0.45	0.92	0.29	0.09	0.45
		RM 7-DD	0.64	0.46	0.98	0.29	0.08	0.46
Concentration in sediment porewater (CSD)	ng/g	site wide	4.9E-06	3.4E-06	7.6E-06	2.9E-06	1.3E-06	5.7E-06
		RM 4-DD	7.5E-06	4.6E-06	1.0E-05	3.1E-06	9.7E-07	4.7E-06
		RM 7-DD	7.4E-06	5.2E-06	1.2E-05	3.1E-06	8.7E-07	4.8E-06
Bioavailable concentration in water (CWB)	ng/g	site wide	5.2E-07	3.1E-08	6.0E-07	1.9E-07	9.5E-08	3.6E-07
		RM 4-DD	2.4E-07	1.2E-08	8.8E-07	7.0E-08	1.7E-08	4.0E-07
		RM 7-DD	1.9E-07	4.2E-08	8.8E-07	5.3E-08	1.1E-08	3.6E-07
Concentration in water column particulates (CPART)	ng/g dw	site wide	0.23	0.08	0.58	0.19	0.09	0.37
		RM 4-DD	0.25	0.09	0.90	0.09	0.01	0.43
		RM 7-DD	0.22	0.03	0.99	0.07	0.006	0.40
Concentration in near-bottom particulates (CPART_DET)	ng/g dw	site wide	0.22	0.06	0.96	0.20	0.08	0.58
		RM 4-DD	0.26	0.04	0.90	0.10	0.01	0.46
		RM 7-DD	0.22	0.02	0.99	0.07	0.006	0.43

DD – Dundee Dam

RM – river mile

TCDD – tetrachlorodibenzo-*p*-dioxin

**Table 2-2. Chemical-specific parameter values for tetraCB**

Parameter Name		Spatial Segment	River-wide Parameter Values for TetraCB			Mudflats-only Parameter Values for TetraCB		
			Average	Minimum	Maximum	Average	Minimum	Maximum
Concentration in sediment solids (CST)	ng/g dw	site wide	232	193	359	232	164	368
		RM 4-DD	229	178	355	198	93	281
		RM 7-DD	217	156	306	190	81	277
Concentration in porewater (CSD)	ng/g	site wide	2.4E-03	1.4E-03	5.0E-03	2.4E-03	1.4E-03	4.5E-03
		RM 4-DD	3.0E-03	1.6E-03	6.1E-03	3.4E-03	1.8E-03	5.6E-03
		RM 7-DD	3.2E-03	1.7E-03	5.6E-03	3.4E-03	1.9E-03	5.7E-03
Bioavailable concentration in water (CWB)	ng/g	site wide	6.0E-04	3.5E-04	1.1E-03	6.1E-04	4.1E-04	8.8E-04
		RM 4-DD	5.8E-04	2.7E-04	1.4E-03	5.7E-04	3.7E-04	1.0E-03
		RM 7-DD	5.4E-04	2.5E-04	1.4E-03	5.6E-04	3.7E-04	1.0E-03
Concentration in water column particulates (CPART)	ng/g dw	site wide	216	127	373	228	146	313
		RM 4-DD	237	106	493	181	90	324
		RM 7-DD	284	93	504	169	80	294
Concentration in near-bottom particulates (CPART_DET)	ng/g dw	site wide	213	124	368	250	143	996
		RM 4-DD	240	100	502	186	84	339
		RM 7-DD	290	90	515	172	73	308

DD – Dundee Dam

RM – river mile

**Table 2-3. Non-chemical-specific parameter values**

Parameter Name	Spatial Segment	River-wide Parameter Values			Mudflat-only Parameter Values		
		Average	Minimum	Maximum	Average	Minimum	Maximum
Mean water temperature (°C) (TW)	site wide	13.3	1.3	26.2	13.8	1.4	25.2
	RM 4-DD	13.5	0.7	26.6	13.8	0.7	27.5
	RM 7-DD	13.6	0.7	26.8	13.8	0.7	27.6
Organic carbon content of sediment (fraction) (OCSS)	site wide	0.057	0.053	0.060	0.058	0.056	0.061
	RM 4-DD	0.046	0.043	0.050	0.037	0.034	0.039
	RM 7-DD	0.041	0.040	0.043	0.035	0.034	0.037
Organic carbon content of water column particulate (fraction) (OCPART)	site wide	0.13	0.07	0.15	0.13	0.08	0.15
	RM 4-DD	0.16	0.06	0.20	0.13	0.06	0.21
	RM 7-DD	0.18	0.06	0.24	0.13	0.05	0.21
Organic carbon content of near-bottom particulate (fraction) (OCPART_DET)	site wide	0.14	0.07	0.24	0.27	0.12	0.41
	RM 4-DD	0.18	0.07	0.23	0.28	0.10	0.43
	RM 7-DD	0.21	0.06	0.28	0.25	0.08	0.41

DD – Dundee Dam

RM – river mile

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Preliminary

**ATTACHMENT 3. DEVELOPMENT OF  
2,3,7,8-TCDD METABOLIC RATE ASSUMPTIONS**

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**Preliminary**

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## 1 Introduction

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This attachment discusses the development of 2,3,7,8-TCDD metabolic rate distributions for use in the bioaccumulation model and describes the metabolic rate information available for 2,3,7,8-tetrachlorodibenzo-*p*-dioxin (TCDD) for both fish and invertebrates (including both blue crab and small benthic invertebrates).

## 2 Metabolic Rates for Fish

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Fish metabolic rates for 2,3,7,8-TCDD for use in the bioaccumulation model were developed using three main sources:

- **Precedence** – The use of metabolic rates in previous bioaccumulation models were considered.
- **Review of empirical tissue data from the Lower Passaic River Study Area (LPRSA)** – Empirical tissue data were evaluated to determine whether different species uptake and/or metabolize chemicals differently.
- **Available information in literature** – Available information in literature was reviewed to evaluate whether 2,3,7,8-TCDD is metabolized by various species, or whether metabolic biotransformation might serve as a surrogate for other unspecified processes that reduce 2,3,7,8-TCDD uptake, and to select metabolic biotransformation rate constants for use in the LPRSA bioaccumulation model. Arnot et al. (2008a) compiled a database of fish biotransformation rates, which was used as the primary source for assigning metabolic biotransformation rate constants for the LPRSA bioaccumulation model. This paper presented a comprehensive review of available laboratory data on the metabolic biotransformation of non-ionic organic chemicals by fish and also provided and applied methodology for estimating metabolic biotransformation rate constants from the data.

Table 2-1 provides a summary of the selected metabolic biotransformation rate uncertainty distributions and the rationale for the development of these distributions. More details are provided in the subsections that follow.

**Table 2-1. Summary of fish metabolic biotransformation rate distributions**

Chemical	Species	K <sub>M</sub> Distribution		Summary of Rationale
		Nominal Value	Range	
2,3,7,8-TCDD	carp	0.014	0.0016 – 0.056	Species-specific information was available for carp, so metabolic rates were calibrated separately from those for other fish using carp-specific values from Arnot et al. (2008a).
	American eel	0.04	0.0016 – 0.082	Available literature and the LPRSA empirical data indicated that the bioaccumulation pattern for eel is different than those for other fish. No eel-specific metabolic rate data were available; thus, high-end estimates of metabolism were derived using all fish data from Arnot et al. (2008a).
	other fish	0.013	0.007 – 0.024	Metabolic rates were developed using all available metabolic rates for 2,3,7,8-TCDD (i.e., rates for all available species) from Arnot et al. (2008a).

K<sub>M</sub> – metabolism information rate constant

LPRSA – Lower Passaic River Study Area

na – not applicable

TCDD – tetrachloro-dibenzo-*p*-dioxin

When species-specific metabolic biotransformation rate constants were provided in Arnot et al. (2008a) they were applied to the appropriate species in the bioaccumulation model. This was the case for carp and 2,3,7,8-TCDD, for which species-specific estimated rate constants were available from three studies (Arnot et al. 2008b). For carp, the nominal value of the distribution was set equal to the average of the best estimate for the three carp-specific studies (Table 2). The range of the distribution was set equal to the range of the estimated 2.5<sup>th</sup> to 97.5<sup>th</sup> percentile values. Species-specific rate estimates were not available for any other modeled fish species. For all other fish (with the exception of eels as discussed below), the nominal value of the distribution was set equal to the average of the best estimates for all species, and the range was set equal to the minimum and maximum best estimates for all fish species reported in Arnot et al. (2008a) (Table 2-2).

**Table 2-2. Fish metabolic biotransformation rate constants for 2,3,7,8-TCDD Arnot et al. (2008a)**

Species	Best Estimate		Estimated Percentiles		Data Category <sup>a</sup>
	log K <sub>M</sub>	K <sub>M</sub>	2.5 <sup>th</sup> Percentile	97.5 <sup>th</sup> Percentile	
Common carp	-1.72	0.019	0.0063	0.048	1
	-1.85	0.014	0.0044	0.048	1
	-2.12	0.008	0.0016	0.035	1
Fathead minnow	-2.05	0.009	0.0030	0.027	1
	-2.14	0.007	0.0022	0.024	1
Guppy	-2.08	0.008	0.0016	0.044	1
Rainbow trout	-1.62	0.024	0.0071	0.082	1

<sup>a</sup> A data category ranging from 1 (indicating a very high level of confidence) to 5 (indicating a low level of confidence) or 6 (indicating an uncertain level of confidence) was assigned to each study (Arnot et al. 2008b).

$K_M$  – metabolism transformation rate constant reported in Arnot et al. (2008a) are normalized for a 10 g fish at 15°C. The uncertainty ranges on the normalized  $K_M$  values is assumed to be broad enough to capture variability in organism size and water temperature.

TCDD – tetrachlorodibenzo-*p*-dioxin

As noted above, a different metabolic rate distribution was used for American eel and 2,3,7,8-TCDD. Although no species-specific metabolic rate information was available for American eel (*Anguilla rostrata*) in Arnot et al. (2008b) (Table 2), LPRSA empirical tissue data and other literature information discussed below (Van der Oost et al. 1996) support the use of a different metabolic rate for American eel than for other species.

For each species evaluated in the bioaccumulation model, the ratio of the average empirical tissue concentration to the sediment concentration in the applicable modeling area was calculated. These ratios were compared to evaluate whether the bioaccumulation potential and/or metabolism may be different for the various species. The results of this comparison are presented in Table 2-3, which is ordered based on the ratio of tissue to sediment concentrations (highest for carp and lowest for American eel). Some of the differences in these ratios can be explained by the diets of these fish. For example, carp diets are closely tied to sediment (i.e., carp feed by foraging in the sediment for food and thus their diet is composed primarily of sediment, near-bottom particulates, and benthic invertebrates). On the other hand, bass diets are less closely linked to sediment (and more closely linked to water column exposures) because their diet is composed of a higher fraction of small fish and higher-trophic-level benthic invertebrates. Other differences, such as the low ratio for American eel, may indicate that bioaccumulation potential and/or metabolism is different among species.

**Table 2-3. Ratios of fish tissue to sediment concentrations for 2,3,7,8-TCDD in the LPRSA**

Species Group	Average Tissue Concentration (ng/kg ww)	Modeling Area	Sediment SWAC (ng/kg dw)	Ratio of Tissue to Sediment Concentrations
Carp	430	RM 7 – Dundee Dam	1,468	0.29
White perch	130	site-wide	1,000	0.13
Catfish	130	RM 4 – Dundee Dam	1,468	0.09
Bass	30	RM 7 – Dundee Dam	1,468	0.04
American eel	18	site-wide	1,000	0.018

dw – dry weight

LPRSA – Lower Passaic River Study Area

RM – river mile

SWAC – spatially weighted average concentration

ww – wet weight

In a study of the bioaccumulation patterns of various organic compounds in European eel (*Anguilla anguilla*) (a species closely related to American eel) (Van der Oost et al. 1996), the bioaccumulation of dioxins/furans was found to be extremely low. Van der

Oost et al. (1996) concluded that this result was most likely due to reduced uptake, effective metabolic clearance, or both. Although this study was not sufficient to develop an American eel-specific metabolic rate, it supports the use of a different (i.e., higher) metabolic biotransformation rate coefficient for eel relative to the other evaluated fish species.

Thus, based on LPRSA empirical tissue data and the available literature information, a distribution that reflected the higher metabolic biotransformation (or lower uptake) potential for American eel was developed. The nominal value for the American eel distribution was set equal to the average of the 97.5<sup>th</sup> percentile estimates for the available metabolic biotransformation rate constants from Arnot et al. (2008a), and the distribution range reflects the 2.5<sup>th</sup> and 97.5<sup>th</sup> percentiles reported for any species (Arnot et al. 2008a) (Table 2-2).

### 3 Metabolic Biotransformation Rate Constants for Invertebrates

This section presents the selected metabolic biotransformation rate constants for invertebrates and the process used to develop these rate constants. The metabolic biotransformation rate constants for invertebrates (including both small benthic invertebrates and blue crab) were developed based on two main sources:

- **Precedent** – Metabolic biotransformation rate constants used in previous bioaccumulation models were considered.
- **Literature review** – A review of the available literature was conducted for both dioxins and PCBs for invertebrates (details of these searches are provided later in this section).

A summary of the selected 2,3,7,8-TCDD metabolic biotransformation rate constant and rationales is presented in Table 3-1. Additional details are provided in the subsections that follow.

**Table 3-1. Summary of invertebrate metabolic biotransformation rate constant distributions**

Chemical	Species	K <sub>M</sub> Distribution		Summary of Rationale
		Nominal Value	Range	
2,3,7,8-TCDD	small benthic invertebrates	0.013	0.007 – 0.024	The available literature indicated that invertebrates (including both benthic invertebrates and blue crab) may be able to metabolize dioxins/furans. No invertebrate-specific rates were available, and thus the distribution for "other fish" (Table 2-1) was also applied to invertebrates.
	blue crab			

K<sub>M</sub> – metabolism transformation rate constant

na – not applicable

TCDD – tetrachlorodibenzo-*p*-dioxin

Support for the metabolism (or inefficient uptake) of dioxins/furans by invertebrates can be found in work performed for the Contaminant Assessment and Reduction Project (CARP) for the New York / New Jersey Harbor estuary (HydroQual 2007). In that study, biota-sediment accumulation factors (BSAFs) for PCB homologues and dioxin/furan congeners for blue crab, clams, and worms were calculated using field-collected tissue data and model-calculated sediment concentrations. The resulting BSAFs were plotted against  $K_{ow}$  for the two chemical groups (i.e., PCBs and dioxins/furans). The calculated BSAFs for dioxin/furan congeners for clams, crabs, and worms were approximately 10 times lower than those for PCBs (for chemicals with similar  $K_{ow}$ s). The HydroQual (2007) report stated that “this suggests that either there is inefficient transfer of dioxin/furan congeners from sediment, or that worms also possess the capacity to metabolize dioxin and furan congeners.” A similar summary was provided in the same report for clam and crab.

The HydroQual (2007) report did not include metabolism by zooplankton based on a similar comparison of empirical tissue concentrations and modeled dissolved water concentrations for PCBs and dioxins/furans. This is consistent with the assumption that the metabolic rate for zooplankton is equal to 0 in the LPRSA bioaccumulation model.

As part of the effort to develop metabolism biotransformation rate constants for 2,3,7,8-TCDD, a literature search was conducted in September 2014 for studies on the metabolism of dioxins and furans by aquatic invertebrates using the Web of Science database. Search terms used in this search included dioxin, furan, metabolism, metabolites, metabolic transformation, biotransformation, crayfish, crab, aquatic organism, biota, and bioaccumulation.

CYP450 1A expression (CYP450 1A1 is the most important enzyme in TCDD metabolism for vertebrates) is not known to occur in benthic invertebrates. It is possible that benthic invertebrates metabolize 2,3,7,8-TCDD by a different route than vertebrates. One study (Zhang et al. 2011), which measured the uptake and elimination of a dioxin compound for invertebrates, was found. In this study, radiotracers were used to measure the uptake, assimilation efficiency, and elimination of 1,2,3,4,7,8-hexachlorodibenzo-*p*-dioxin<sup>1</sup> in marine phytoplankton, copepods, and fish. The half-life of 1,2,3,4,7,8-hexachlorodibenzo-*p*-dioxin of 2 to 25 days for copepods was lower than that observed for fish in other studies (Zhang et al. 2011). According to Zhang et al. (2011), the results suggested that these invertebrates have rapid metabolic biotransformation rate due to their small size and might indicate that copepods have an efficient elimination system for removing or metabolizing 1,2,3,4,7,8-hexachlorodibenzo-*p*-dioxin.

<sup>1</sup> Zhang et al. (2011) did not identify the specific dioxin compound that was evaluated in this study. In a personal communication, the authors (Wang 2014) clarified that the compound used in their study was 1,2,3,4,7,8-hexachlorodibenzo-*p*-dioxin.

Based on the supporting information summarized above, non-zero metabolic rates were applied for 2,3,7,8-TCDD for both benthic invertebrates and blue crab. No invertebrate-specific rates could be identified so a value was selected from the metabolic bioaccumulation rate constant distribution for fish for small benthic invertebrates and blue crab.

## **Related Processes that Influence Chemical Concentrations**

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When reviewing metabolic biotransformation rate data, it is important to recognize that other processes that influence chemical concentrations in biota are likely to affect these data. In a study of European eel, Van der Oost et al. (1996) noted that the lower chemical concentrations observed in eel could be the result of reduced uptake, high rates of metabolism, or a combination of these processes. For the purpose of the LPRSA bioaccumulation model, it is not necessarily important to distinguish between the metabolic biotransformation rate and factors that could reduce the uptake of a given chemical because both processes have the same outcome: a lower concentration of the chemical (i.e., parent or unmetabolized chemical) in biota tissue. However, it is important to acknowledge the overlapping nature of these processes, particularly for parameters such as the metabolic biotransformation rate constant, for which species-specific and / or site-specific data are often unavailable.

Rather than attempting to capture all of the processes that exist in a system (a task that would be nearly impossible to properly parameterize), the goal of the bioaccumulation model is to replicate the LPRSA system to the extent necessary to accurately predict tissue concentrations. It is important to add sufficient complexity to ensure that the model can replicate the complex natural system and at the same time not create an unnecessarily complex model. Thus, in cases where chemical-specific metabolic rates and other factors result in a reduced uptake of chemicals, it is appropriate to use a single parameter to act as a surrogate for related processes.

## **5 References**

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## ATTACHMENT 4. DEVELOPMENT OF DIETARY ASSUMPTIONS FOR FISH AND CRAB

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Preliminary

# 1 Introduction

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For the species or species groups included in the bioaccumulation model and / or evaluated in the Lower Passaic River Study Area (LPRSA) baseline ecological risk assessment (BERA) (Windward [in prep]), diets were assigned based on a review of regional and general scientific literature. LPRSA life history profiles, included as Appendix A of the revised risk analysis and risk characterization (RARC) plan (Windward and AECOM [in prep]), presented general data from the literature regarding the life histories and potential diets of LPRSA ecological receptors. This appendix presents the details of the development of those dietary assumptions (i.e., the dietary items included and the portions of each prey item).

For species for which diets were used in both in the bioaccumulation model and in the evaluation of risk in the BERA, the dietary assumptions were developed to be consistent with one another. However, the way in which these diets were applied for the BERA and the bioaccumulation model were somewhat different for the following reasons:

- **Limited species for which empirical data were available** – For the BERA (Windward [in prep]), dietary components were limited to those prey types for which empirical LPRSA chemistry data were available (i.e., sediment, benthic invertebrate [worm] tissue from bioaccumulation testing, blue crab tissue, and fish tissue). Dietary components for the bioaccumulation model were limited to the modeled species/species groups, which included a wider range of potential dietary or prey items (e.g., particulate/detritus, phytoplankton/algae, and zooplankton), and specific invertebrate compartments (i.e., small benthic invertebrate deposit feeders [DEP], small benthic invertebrate detritivores [DET], and benthic invertebrate carnivores/omnivores [C/O]) with bioaccumulation model-estimated concentrations.
- **Ability to incorporate ranges in the bioaccumulation model** – Although the bioaccumulation model used point estimates for prey portions, as did the BERA (Windward [in prep]), the development of the bioaccumulation model also involved the characterization of ranges for each prey item. These ranges were intended to account for both the uncertainty of the assigned percentages (given the site-specific opportunistic feeding behavior of fish) and the variability of the diets depending on prey availability (i.e., the season and specific location within the LPRSA of a given fish may result in a significantly different diet).
- **Inclusion of sediment in the diet** – The bioaccumulation model included sediment (as sediment solids or particulate/detritus) as an explicit component of the diet. Sediment was treated as an incidental contributor to exposure in the BERA.

Particulate/ detritus was not a dietary portion that could be explicitly included in the LPRSA BERA dietary calculations because empirical chemical concentration data were not available for particulates/ detritus, and (as noted above) only empirical data were used to derive dietary concentrations for the BERA.

The dietary assumptions for fish and blue crab are summarized in Table 1. A detailed rationale for the development of these diets is presented in Table 2.

**Table 1. General comparison of BERA and bioaccumulation model fish prey composition**

Fish Species	Dietary Items and Portions		Notes
	LPRSA BERA	LPRSA Bioaccumulation Model	
Filter feeding fish (Atlantic menhaden)	species not evaluated in BERA	50% particulates/detritus 25% zooplankton/algae 25% zooplankton	na
Small forage fish (mummichog)	100% worms	1% sediment solids 15% particulates/ detritus 1% phytoplankton/algae 1% zooplankton 65% benthic invertebrates	Of the available empirical data for the BERA, only worms were appropriate as a dietary item for small forage fish. In the BERA, worms were in part used as a surrogate for the consumption of particulates/detritus, phytoplankton/ algae, and zooplankton. In addition, sediment was included as an incidentally ingested component in the BERA, rather than as a part of the overall diet.
Blue crab	species not evaluated in the BERA	2% sediment solids 1% particulates/detritus 83% benthic invertebrates 14% small fish	na
Carp	species not evaluated in BERA	15% sediment solids 25% particulates/detritus 5% phytoplankton/algae 54% invertebrates 1% small fish	na
Catfish	channel catfish specifically evaluated in BERA: 55% worms 5% blue crab 40% small fish	5% sediment solids 10% particulates/detritus 2% phytoplankton/algae 43% benthic invertebrates 40% small fish	Diets included the same portion of small fish. The invertebrate portion of the diet in the BERA (worms and blue crab) was in part used as a surrogate for the consumption of particulates/detritus and phytoplankton/algae. In addition, sediment was included as an incidentally ingested component in the BERA, rather than as a part of the overall diet.
White perch	70% worms 15% blue crab 15% small fish	5% particulates/detritus 2% phytoplankton/algae 3% zooplankton 75% benthic invertebrates 15% small fish	Diets included the same portion of small fish. The invertebrate portion of the diet in the BERA (worms and blue crab) was in part used as a surrogate for the consumption of particulates/detritus, phytoplankton/algae and zooplankton.
American eel < 50 cm	80% worms 10% blue crab 10% small fish	small American eel not evaluated in the bioaccumulation model	na

**Table 1. General comparison of BERA and bioaccumulation model fish prey composition**

Fish Species	Dietary Items and Portions		Notes
	LPRSA BERA	LPRSA Bioaccumulation Model	
Amia (largemouth and smallmouth) > 50 cm	35% worms 25% blue crab 40% small fish	2% sediment solids 3% particulates/detritus 55% benthic invertebrates 40% small fish	Diets included the same portion of small fish. The invertebrate portion of the diet in the BERA (worms and blue crab) was in part used as a surrogate for the consumption of particulates/detritus. In addition, sediment was included as an incidentally ingested component in the BERA, rather than as a part of the overall diet.
Bass (largemouth and smallmouth)	10% worms 10% blue crab 80% small fish	20% benthic invertebrates 80% small fish	Diets included the same portion of small fish and invertebrates (represented by worms and blue crab in the BERA). In addition, sediment was included as an incidentally ingested component in the BERA, rather than as a part of the overall diet.

BERA – baseline ecological risk assessment

LPRSA – Lower Passaic River Study Area

na – not applicable

Table 2. Rationale for BERA and bioaccumulation model fish prey composition assumptions

Dietary Information and Prey Portions from Literature	BERA Prey Portions		Bioaccumulation Model Prey Portions	
	Options for BERA Parameters	Selected BERA Prey Portions/Rationale	Prey Portion Options	Selected Diet and Rationale
<b>Filter-Feeding Fish (Atlantic menhaden)</b>  Menhaden are opportunistic filter feeders as both juveniles and adults. Based on data from the mid-Atlantic and New England areas, menhaden consume the following, the proportions of which depend on prey availability (Rogers and Vanden Avyle 1975): <ul style="list-style-type: none"><li>Amorphous material (majority of their prey)</li><li>Zooplankton (zooplankton portion of the diet decreases as fish move from open waters to marshes)</li><li>Phytoplankton/diatom chains (if phytoplankton abundance is limited, may consume more detritus)</li></ul> Both juveniles and adults are filter feeders. Food items include the following based on data from the East Coast (FishBase 2014): <ul style="list-style-type: none"><li>46 – 81% detritus</li><li>0 – 36% phytoplankton</li><li>18 – 20% zooplankton (copepods)</li></ul>	<i>Species not evaluated in BERA; not selected as an ecological receptor for evaluation.</i>	<b>Species not evaluated in BERA; not selected as an ecological receptor for evaluation.</b>	<ul style="list-style-type: none"><li>Particulates/detritus</li><li>Phytoplankton/algae</li><li>Zooplankton (representing copepods) (Quantitative data not available)</li></ul> <ul style="list-style-type: none"><li>46 – 81% particulates/detritus</li><li>0 – 36% phytoplankton/algae</li><li>18 – 20% zooplankton (representing copepods)</li></ul>	<b>Based on the available information and the fact that menhaden are opportunistic filter feeders, approximately half of the diet was assumed to be particulates/detritus, with the remainder assumed to be phytoplankton/algae and zooplankton:</b> <ul style="list-style-type: none"><li>50% particulates/detritus (water-column)</li><li>25% phytoplankton/algae</li><li>25% zooplankton</li></ul> <b>Calibration ranges are based on general ranges available from literature.</b>
<b>Small Forage Fish (mummichog)</b>  LPRSA-specific empirical data are not available; reported prey items from various studies throughout the East Coast, including New Jersey, Connecticut, New England and mid-Atlantic states (Abraham 1985; Allen et al. 1994; James-Pirri et al. 2001; Kneib 1986; Currin et al. 2003) include the following: <ul style="list-style-type: none"><li>Detritus</li><li>Algae</li><li>Small crustaceans (amphipods, tanaids, copepods, and ostracods)</li><li>Polychaetes</li><li>Insects (adult and larvae)</li></ul> Mummichogs are bottom feeders. Food items for juveniles and adults include the following (dietary proportions are not provided (FishBase 2014): <ul style="list-style-type: none"><li>Benthic invertebrates (benthic crustaceans, worms, mollusks)</li><li>Insects</li><li>Small fish</li></ul>	<ul style="list-style-type: none"><li>Worms (invertebrate and insect surrogate) (Quantitative data not available)</li></ul> <ul style="list-style-type: none"><li>Worms (invertebrate and insect surrogate)</li><li>Small fish (Quantitative data not available)</li></ul>	<b>Not composed of only prey for which empirical data were available from the LPRSA: 100% worms (surrogate for invertebrate and insects; also representing consumption of detritus, algae, and zooplankton)</b>  <b>Small fish were not expected to comprise a meaningful proportion of the diet.</b>	<ul style="list-style-type: none"><li>Sediment solids</li><li>Particulates/detritus</li><li>Phytoplankton/algae</li><li>Zooplankton (representing copepods)</li><li>Benthic invertebrates (Quantitative data not available)</li></ul> <ul style="list-style-type: none"><li>Benthic invertebrates (Quantitative data not available)</li></ul>	<b>Based on prey items listed in literature and the assumption that they feed primarily on benthic invertebrates, with some incidental detritus ingestion, the representative bioaccumulation model compartments were assigned the following prey portions:</b> <ul style="list-style-type: none"><li>1% sediment solids</li><li>15% particulates/detritus (near-bottom)</li><li>15% phytoplankton/algae</li><li>4% zooplankton</li><li>65% benthic invertebrates (consumed proportionally to LPRSA biomass)</li></ul> <b>Small fish not expected to comprise a meaningful proportion of the diet. Calibration ranges are based on professional judgment.</b>

**Table 2. Rationale for BERA and bioaccumulation model fish prey composition assumptions**

Dietary Information and Prey Portions from Literature	BERA Prey Portions		Bioaccumulation Model Prey Portions	
	Options for BERA Parameters	Selected BERA Prey Portions/Rationale	Prey Portion Options	Selected Diet and Rationale
<p><b>Blue Crab</b></p> <p>A study of blue crab feeding habits conducted in a northern Florida estuary found that the diets of larger blue crab were directly influenced by prey availability. This study found the following average diets for blue crab larger than 6 cm (Laughlin 1982):</p> <ul style="list-style-type: none"> <li>• 73% benthic invertebrates (39% bivalves, 24% crab, 5% shrimp, 4% gastropods)</li> <li>• 14% small fish</li> <li>• 3% plant matter</li> <li>• other diet portions reported included various remains (animal, crab, and crustaceans), detritus, sand grains, and insect larva</li> </ul> <p>A Raritan Bay study that evaluated the stomach contents of over 400 blue crab reported the following average percents by volume (Stehlik et al. 1998). The study noted that unlike in other studies, small fish were not found in the blue crab stomachs.</p> <ul style="list-style-type: none"> <li>• 44% mollusks</li> <li>• 40% crabs</li> <li>• 1% polychaetes</li> <li>• 15% other unidentified matter</li> </ul> <p>A study conducted in the Rhodes River (Hines et al. 1990), an estuary of the Chesapeake Bay, reported the following stomach content percentages for crabs that averaged 13 cm in length:</p> <ul style="list-style-type: none"> <li>• 2% sediment (range of 0 to 5%)</li> <li>• 1% detritus (range of 0 to 2%)</li> <li>• 67% invertebrates (range of 62 to 71%), comprised primarily of clams and crabs</li> <li>• 12% fish (range of 4 to 17%)</li> <li>• 18% other digested animal tissue (range of 9 to 21%)</li> </ul>	<p>Species not evaluated in BERA; not selected as an ecological receptor for evaluation.</p>	<p>Species not evaluated in BERA; not selected as an ecological receptor for evaluation.</p>	<p>Study by Laughlin (1982) was considered qualitatively because the crab evaluated were smaller than those evaluated in the LPRSA.</p> <ul style="list-style-type: none"> <li>• 1% sediment solids</li> <li>• 11% particulates/detritus</li> <li>• 73% benthic invertebrates</li> <li>• 14% small fish</li> </ul> <p>Study by Stehlik et al. (1998) was considered qualitatively because the size class was not known.</p> <ul style="list-style-type: none"> <li>• 15% particulates/detritus</li> <li>• 85% benthic invertebrates</li> </ul> <p>Aggregating the data reported by Hines et al. (1990):</p> <ul style="list-style-type: none"> <li>• 2% sediment solids</li> <li>• 1% particulates/detritus</li> <li>• 83% benthic invertebrates</li> <li>• 14% fish</li> </ul> <p>(Note – Portion of diet composed of digested animal tissue divided proportionally between benthic invertebrates and fish.)</p>	<p>Diet was based primarily on Hines et al. (1990) because the crab in that study most closely matched the size of crab being modeled:</p> <ul style="list-style-type: none"> <li>• 2% sediment solids</li> <li>• 1% particulates/detritus (near-bottom)</li> <li>• 83% benthic invertebrates (consumed proportionally to LPRSA biomass)</li> <li>• 14% small fish</li> </ul> <p>Calibration ranges were based on the ranges reported by Hines et al. (1990) and PROFESSIONAL JUDGMENT using qualitative information from other literature studies.</p>
<p><b>Common Carp</b></p> <p>Carp are highly opportunistic feeders with a variable diet. The majority of the diet is composed of the following components (Maryland DNR 2007; Garcia-Berthou 2001; USGS 2010; Walburg and Nelson 1966):</p> <ul style="list-style-type: none"> <li>• Detritus</li> <li>• Algae/plants</li> <li>• Small benthic invertebrates</li> </ul> <p>Carp may also consume:</p> <ul style="list-style-type: none"> <li>• Insects</li> <li>• Small fish</li> <li>• Zooplankton</li> </ul>	<p>Species not evaluated in BERA; not selected as an ecological receptor for evaluation.</p>	<p>Species not evaluated in BERA; not selected as an ecological receptor for evaluation.</p>	<ul style="list-style-type: none"> <li>• Sediment solids</li> <li>• Particulates/detritus</li> <li>• Algae/plants</li> <li>• Phytoplankton/zooplankton</li> <li>• Benthic invertebrates</li> <li>• Small fish</li> </ul> <p>(Qualitative data not available.)</p>	<p>Selected diet for carp was based on general adult diet portions from the literature (regional data were not available). Diet also accounted for the benthic feeding habits of carp (i.e., high incidental sediment and detritus ingestion), and limited abundance of phytoplankton/algae in the LPRSA relative to other prey (i.e., portion of phytoplankton/algae was decreased relative to other more abundant prey items). The representative</p>

Table 2. Rationale for BERA and bioaccumulation model fish prey composition assumptions

Dietary Information and Prey Portions from Literature	BERA Prey Portions		Bioaccumulation Model Prey Portions	
	Options for BERA Parameters	Selected BERA Prey Portions/Rationale	Prey Portion Options	Selected Diet and Rationale
<p>Common dietary items for carp in Colorado waters include the following (FishBase 2014)(ranges are based on percentages reported for three different areas):</p> <ul style="list-style-type: none"><li>• 24 – 56% detritus (average = 37%)</li><li>• 22 – 60% plants/benthic algae (average = 36%)</li><li>• 0 – 2% zooplankton (average = 1%)</li><li>• 4 – 11% insects (average = 8%)</li><li>• 2 – 44% benthic invertebrates (e.g., crayfish) (average = 17%)</li><li>• 0 – 2% fish (average = 1%)</li></ul>			<p>Information from FishBase (2014) can be aggregated as follows:</p> <ul style="list-style-type: none"><li>• 24 – 56% sediment solids plus particulates/detritus</li><li>• 22 – 60% phytoplankton/algae (representing plants/benthic algae)</li><li>• 0 – 2% zooplankton</li><li>• 6 – 54% benthic invertebrates (representing benthic invertebrates and insects)</li><li>• 0 – 2% fish</li></ul>	<p>Bioaccumulation model compartments were assigned the following prey portions:</p> <ul style="list-style-type: none"><li>• 15% sediment solids</li><li>• 25% particulates/detritus (near-bottom)</li><li>• 5% phytoplankton/algae</li><li>• 54% invertebrates (consumed proportional to abundance in the LPRSA)</li><li>• 1% small fish (benthic forage fish)</li></ul> <p>Calibration ranges were based on general ranges available from literature and PROFESSIONAL JUDGMENT.</p>



Table 2. Rationale for BERA and bioaccumulation model fish prey composition assumptions

Dietary Information and Prey Portions from Literature	BERA Prey Portions		Bioaccumulation Model Prey Portions	
	Options for BERA Parameters	Selected BERA Prey Portions/Rationale	Prey Portion Options	Selected Diet and Rationale
<b>White Perch</b> Food items for white perch included the following (dietary proportions were not provided) (FishBase 2014): <ul style="list-style-type: none"><li>• Insects</li><li>• Fish eggs/fish</li><li>• Detritus</li><li>• Benthic invertebrates (amphipods, annelids, mollusks)</li><li>• Cladocerans</li></ul> Hackensack River (New Jersey) study reported the stomach contents for 78 white perch as percent dry weight (Weis 2005): <ul style="list-style-type: none"><li>• 23% amphipods</li><li>• 17% shrimp</li><li>• 17% fish</li><li>• &lt; 1% plant matter</li><li>• 43% unidentified material</li></ul> Study of white perch in the Hudson River (New York) that reported the frequency of occurrence of prey items in white perch stomachs (Bath and O'Connor 1985). The following percentages are estimates based on mature white perch (> 11 cm in length): <ul style="list-style-type: none"><li>• 54% benthic invertebrates (6% annelid worms [seasonal range of 0 – 10%]; 40% amphipods [seasonal range of 25 – 75%]; 8% isopods [seasonal range of 0 – 25%])</li><li>• 1% insects (seasonal range of 0 – 5%)</li><li>• 5% shrimp (seasonal range of 0 – 20%)</li><li>• 4% fish / fish larvae (seasonal range not provided)</li><li>• 9% plant matter (seasonal range of 0 – 25%)</li><li>• 30% unidentified material (seasonal range not provided)</li></ul> Study of white perch in the York River (Virginia) that reported the approximate percent composition of white perch diet by weight for 12 mature white perch (McGrath 2005): <ul style="list-style-type: none"><li>• 85% decapods (68% crab [mud, blue, and fiddler crab], 17% shrimp)</li><li>• 6% hydroid</li><li>• 5% seahorse</li><li>• 4% other benthic invertebrates (3% amphipods, 1% polychaetes)</li></ul> LPRSA qualitative stomach content material: <ul style="list-style-type: none"><li>• Amphipods</li></ul> Lake Erie study reporting dietary percentages (by volume) of stomach contents for 421 white perch collected from June through September in 1981 (Schaeffer and Margraf 1986): <ul style="list-style-type: none"><li>• 55% zooplankton (48% cladocerans [0 – 96%], 7% copepods [0 – 20%])</li><li>• 7% benthic invertebrates (chironomids [0 – 14%])</li><li>• 38% fish (miscellaneous species [1 – 92%])</li></ul> Value is the average for the 4 months; range is the range of value across the 4 months.	<ul style="list-style-type: none"><li>• worms (benthic invertebrate and insect surrogate)</li><li>• small fish</li><li>• <i>(Quantitative data not available.)</i></li></ul> <ul style="list-style-type: none"><li>• 70% worms (amphipod surrogate)</li><li>• 17% blue crab (shrimp surrogate)</li><li>• 17% small fish</li><li>• 4% other (unidentified material)</li></ul> <ul style="list-style-type: none"><li>• high consumption of worms (invertebrate surrogate for primarily non-crustaceans)</li><li>• low consumption of small fish <i>(Study based on frequency of occurrence; data used qualitatively to assign prey portions.)</i></li></ul> <ul style="list-style-type: none"><li>• 85% blue crab (crab/shrimp surrogate)</li><li>• 10% worms (invertebrate surrogate)</li><li>• 5% other <i>(Study not used to develop diet portions because the available regional data were determined to be more applicable.)</i></li></ul> <ul style="list-style-type: none"><li>• Worm (amphipod surrogate) <i>(Quantitative site-specific data not available.)</i></li></ul> <ul style="list-style-type: none"><li>• 62% worm (invertebrate surrogate)</li><li>• 38% small fish <i>(Study not used to develop diet portions because the available regional data were determined to be more applicable.)</i></li></ul>	<p>Diet determined based on regional data, including quantitative data from the Hackensack River and qualitative data from the Hudson River. Diet composed of only prey for which empirical data were available from the LPRSA:</p> <ul style="list-style-type: none"><li>• 70% worms (surrogate for benthic invertebrates; also representing consumption of detritus, algae, and zooplankton)</li><li>• 15% blue crab (surrogate for small crustaceans; also representing consumption of detritus, algae, and zooplankton)</li><li>• 17% small fish</li></ul> <p>Diet is a best estimate of the year-round white perch diet using the available empirical data, although the diet could be highly variable depending on the season.</p>	<ul style="list-style-type: none"><li>• Detritus</li><li>• Zooplankton</li><li>• Benthic invertebrates</li><li>• Small fish</li><li>• <i>(Quantitative data not available.)</i></li></ul> <ul style="list-style-type: none"><li>• 40% benthic invertebrates (representing amphipods and shrimp)</li><li>• 17% small fish</li><li>• 43% other (unidentified material)</li></ul> <ul style="list-style-type: none"><li>• High consumption of invertebrates (primarily non-crustaceans)</li><li>• Low consumption of small fish <i>(Study based on frequency of occurrence; data used qualitatively to assign prey portions.)</i></li></ul> <ul style="list-style-type: none"><li>• 95% benthic invertebrates</li><li>• 5% other <i>(Study not used to develop diet portions because the available regional data were determined to be more applicable.)</i></li></ul> <ul style="list-style-type: none"><li>• Benthic invertebrates (representing amphipods)</li><li>• 55% zooplankton (cladocerans and copepods)</li><li>• 7% benthic invertebrates (chironomids)</li><li>• 38% small fish <i>(Study not used to develop diet portions because the available regional data were determined to be more applicable.)</i></li></ul>	<p>Selected diet for white perch was based on regional data, including quantitative data from the Hackensack River and qualitative data from the Hudson River. The portion of the diet identified as "unidentified material" was assigned primarily to benthic invertebrates; this portion was assumed to be composed of a small amount of detritus, phytoplankton, and zooplankton based on information from other studies that suggested that perch may consume a small amount of these items when they are available or incidentally while feeding. Although the Lake Erie study reported a high percentage of zooplankton in the white perch diet, zooplankton were assumed to represent a small percentage of the white perch diet in the Passaic River due to the relatively low abundance of zooplankton in the LPRSA. The representative bioaccumulation model compartments were assigned the following prey portions:</p> <ul style="list-style-type: none"><li>• 5% particulates/detritus (near-bottom)</li><li>• 2% phytoplankton/algae</li><li>• 3% zooplankton</li><li>• 75% benthic invertebrates (primarily amphipods and shrimp)</li><li>• 15% small fish (primarily benthic forage fish and some filter-feeding fish)</li></ul> <p>Selected calibration ranges were quite wide based on the opportunistic foraging habits of white perch.</p>

Table 2. Rationale for BERA and bioaccumulation model fish prey composition assumptions

Dietary Information and Prey Portions from Literature	BERA Prey Portions		Bioaccumulation Model Prey Portions	
	Options for BERA Parameters	Selected BERA Prey Portions/Rationale	Prey Portion Options	Selected Diet and Rationale
<b>American Eel &lt; 50 cm</b>				
Dietary portion ranges for American eel < 50 cm in length from New Jersey streams were as follows (Ogden 1970): <ul style="list-style-type: none"><li>• 0 – 19% crustaceans</li><li>• 72 – 100% insects</li><li>• 0 – 22% fish</li></ul>	<ul style="list-style-type: none"><li>• 72 – 100% worms (insect surrogate)</li><li>• 0 – 19% blue crab (crustacean surrogate)</li><li>• 0 – 22% small fish</li></ul>		American eel of this size class were not evaluated in the bioaccumulation model.	
Dietary portion ranges for American eel < 25 cm in length from the James River, tributary to Chesapeake Bay, were as follows (Lookabaugh and Angermeier 1992): <ul style="list-style-type: none"><li>• 95% invertebrates</li><li>• 5% crayfish</li></ul>	<ul style="list-style-type: none"><li>• 95% worms (invertebrate surrogate)</li><li>• 5% blue crab (crayfish surrogate)</li><li><i>(Dietary data not used because data not include fish between 25 and 50 cm in length.)</i></li></ul>	<b>Diet based on general ranges from regional (New Jersey) data for eel &lt; 50 cm in length. Diet composed of only prey for which empirical data were available from the LPRSA:</b> <ul style="list-style-type: none"><li>• 80% worms (insect surrogate)</li><li>• 10% blue crab (surrogare for small crustaceans)</li><li>• 10% small fish</li></ul>	American eel of this size class were not evaluated in the bioaccumulation model.	<b>American eel of this size class were not evaluated in the bioaccumulation model.</b>
Common dietary items for stocked American eel < 50 cm in length in Lake Champlain (Vermont) included the following (FishBase 2014): <ul style="list-style-type: none"><li>• 2% amphipods</li><li>• 2% mollusks</li><li>• 33% insects</li><li>• 30% benthic crustaceans (decapods)</li><li>• 1% plants</li><li>• 32% fish</li></ul>	<ul style="list-style-type: none"><li>• 80% worms (amphipod, mollusk, and insect surrogate)</li><li>• 30% blue crab</li><li>• 32% small fish</li></ul>		American eel of this size class were not evaluated in the bioaccumulation model.	
<b>American Eel ≥ 50 cm</b>				
Dietary portion ranges for American eel > 50 cm in length from New Jersey streams were as follows (Ogden 1970): <ul style="list-style-type: none"><li>• 20 – 40% crustaceans</li><li>• 0 – 40% insects</li><li>• 20 – 60% fish</li></ul>	<ul style="list-style-type: none"><li>• 0 – 40% worms (insect surrogate)</li><li>• 20 – 40% blue crab (crustacean surrogate)</li><li>• 20 – 60% small fish</li></ul>	<b>Diet based on general ranges from regional (New Jersey) data for eel &gt; 50 cm. Diet composed of only prey for which empirical data were available from the LPRSA:</b> <ul style="list-style-type: none"><li>• 80% worms (surrogate for small invertebrates; also representing consumption of detritus)</li><li>• 25% blue crab (surrogate for crayfish/ small crustaceans; also representing consumption of detritus)</li><li>• 40% small fish</li></ul>	<ul style="list-style-type: none"><li>• 20 – 80% benthic invertebrates (representing crustaceans and insects)</li><li>• 20 – 60% small fish</li><li>• 100% benthic invertebrates</li></ul>	<b>Selected diet for American eel was based on general ranges from regional (New Jersey) data for eel &gt; 50 cm, and on PROFESSIONAL JUDGMENT regarding incidental ingestion of sediment solids and particulates/detritus. The representative bioaccumulation model compartments were assigned the following prey portions:</b> <ul style="list-style-type: none"><li>• 2% sediment solids</li><li>• 3% particulates/detritus (near-bottom)</li><li>• 55% benthic invertebrates (primarily crustaceans but also smaller invertebrates)</li><li>• 40% small fish (primarily benthic forage fish and some filter-feeding fish)</li></ul> <b>Calibration ranges were based on general ranges from the literature and PROFESSIONAL JUDGMENT.</b>
Dietary portion ranges for American eel > 37 cm in length from the James River, tributary to Chesapeake Bay, were as follows (Lookabaugh and Angermeier 1992): <ul style="list-style-type: none"><li>• &lt; 5% invertebrates</li><li>• &gt; 95% crayfish</li></ul>	<ul style="list-style-type: none"><li>• 5% worms (invertebrate surrogate)</li><li>• 95% blue crab (crayfish surrogate)</li><li><i>(Dietary data not used because data include fish smaller than 50 cm in length.)</i></li></ul>			
Common dietary items for stocked American eel > 50 cm in length from Lake Champlain (Vermont) included the following (FishBase 2014) <ul style="list-style-type: none"><li>• 1 – 6% amphipods</li><li>• 3– 6% mollusks</li><li>• 25 – 30% insects</li><li>• 18 – 45% benthic crustaceans (decapods)</li><li>• 1% plants</li><li>• 22 – 43% fish</li></ul>	<ul style="list-style-type: none"><li>• 29 – 42% worms (amphipod, mollusk, and insect surrogate)</li><li>• 18 – 45% blue crab</li><li>• 22 – 43% small fish</li></ul>		<ul style="list-style-type: none"><li>• 47 – 87% benthic invertebrates (representing amphipods, mollusks, crustaceans, and insect surrogate)</li><li>• 22 – 43% small fish</li></ul>	

Table 2. Rationale for BERA and bioaccumulation model fish prey composition assumptions

Dietary Information and Prey Portions from Literature	BERA Prey Portions		Bioaccumulation Model Prey Portions	
	Options for BERA Parameters	Selected BERA Prey Portions/Rationale	Prey Portion Options	Selected Diet and Rationale
<b>Bass (smallmouth and largemouth)</b>  Study of largemouth bass in the Hudson River (New York) (USEPA 2006): <ul style="list-style-type: none"><li>• 10 – 25% invertebrates (most commonly occurring were, fish, amphipods, isopods, cladocerans, cyclopoid copepods, ostracods, and some chironomid larvae)</li><li>• 75 – 90% fish</li></ul> Study of smallmouth bass in Lake Sammamish (Washington State) that reported the frequency of occurrence of prey in bass stomachs. Ranges were based on bass age through 5 years (Pflug and Pauley 1984). <ul style="list-style-type: none"><li>• 0 – 19% aquatic insects</li><li>• 15 – 42% crayfish</li><li>• 50 – 71% fish</li></ul> Willamette River study of both largemouth and smallmouth bass that reported the percentage (wet weight) of stomach contents (Pribyl et al. 2005). Smallmouth bass (n = 15): <ul style="list-style-type: none"><li>• 90% fish</li><li>• 5% crayfish</li><li>• 5% shrimp</li></ul> Largemouth bass (n = 5): <ul style="list-style-type: none"><li>• 100% crayfish</li></ul>  Common dietary items for juvenile and adult largemouth bass (16 to 49 cm in length) from California rivers include the following (FishBase 2014): <ul style="list-style-type: none"><li>• 16% benthic invertebrates (crayfish)</li><li>• 51% amphibians</li><li>• 33% small fish</li></ul>  Common dietary items for adult smallmouth bass from Pennsylvania, Minnesota, and California rivers include the following (FishBase 2014): <ul style="list-style-type: none"><li>• 0 – 6% detritus</li><li>• 1 – 92% insects</li><li>• 2 – 21% decapods</li><li>• 0 – 9% other benthic invertebrates (other crustaceans and oligochaetes)</li><li>• 0 – 78% fish</li></ul>	<ul style="list-style-type: none"><li>• 10% worms (benthic invertebrate surrogate)</li><li>• 10% blue crab (crayfish surrogate)</li><li>• 80% small fish</li></ul> <ul style="list-style-type: none"><li>• 10% worms (insect surrogate)</li><li>• 10% blue crab (crayfish surrogate)</li><li>• Small fish</li></ul> <i>(Dietary portions not based on study because regional data were available.)</i>  <ul style="list-style-type: none"><li>• 10 – 100% blue crab (crayfish/shrimp surrogate)</li><li>• 0 – 90% small fish</li></ul> <i>(Dietary portions not based on study because regional data were available.)</i>  <ul style="list-style-type: none"><li>• 16% blue crab (crayfish surrogate)</li><li>• 33% small fish</li><li>• 51% other (amphibians)</li></ul> <i>(Dietary portions not based on study because regional data were available.)</i>  <ul style="list-style-type: none"><li>• 0 – 92% benthic invertebrates (representing, crustaceans, oligochaetes, and insect surrogate)</li><li>• 2 – 21% blue crab (decapod surrogate)</li><li>• 0 – 78% small fish</li></ul> <i>(Dietary portions not based on study because regional data were available.)</i>	<b>Diet based on regional data from the Hudson River. Diet composed of only prey for which empirical data were available from the LPRSA:</b> <ul style="list-style-type: none"><li>• 10% worms (surrogate for amphipod, isopod, and other invertebrates)</li><li>• 10% blue crab (surrogate for crayfish/ all crustaceans)</li><li>• 80% small fish</li></ul>	<ul style="list-style-type: none"><li>• 20% (10-25%) benthic invertebrates</li><li>• 80% (75-90%) small fish</li></ul>  <ul style="list-style-type: none"><li>• Benthic invertebrates (insect and crayfish surrogate)</li><li>• Small fish</li></ul> <i>(Dietary portions not based on study because regional data were available.)</i>  <ul style="list-style-type: none"><li>• 10 – 100% benthic invertebrates (crayfish/ shrimp surrogate)</li><li>• 0 – 90% small fish</li></ul> <i>(Dietary portions not based on study because regional data were available.)</i>  <ul style="list-style-type: none"><li>• 16% benthic invertebrates (representing decapods, other crustaceans, oligochaetes, and insect surrogate)</li><li>• 33% small fish</li><li>• 51% other (amphibians)</li></ul> <i>(Dietary portions not based on study because regional data were available.)</i>  <ul style="list-style-type: none"><li>• 0 – 6% detritus</li><li>• 0 – 92% benthic invertebrates (representing decapods, other crustaceans, oligochaetes, and insect surrogate)</li><li>• 0 – 78% small fish</li></ul> <i>(Dietary portions not based on study because regional data were available.)</i>	<b>Selected diet for bass was based on regional data for largemouth bass from the Hudson River. The representative bioaccumulation model compartments were assigned the following prey portions:</b> <ul style="list-style-type: none"><li>• 20% benthic invertebrates (primarily crayfish and a small portion of amphipods and mollusks)</li><li>• 80% small fish (filter-feeding and benthic forage fish)</li></ul> <b>Broad calibration ranges for the two food items were selected to reflect the known opportunistic nature of bass feeding habits (which may vary greatly depending on season and prey availability).</b>

BERA – baseline ecological risk assessment  
PROFESSIONAL JUDGMENT – best professional judgment  
FWM – food web model  
LPRSA – Lower Passaic River Study Area

## 2 References

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